

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 31, 2006, 09:50:25 ; Search time 46 Seconds
(without alignments)
744.081 Million cell updates/sec

Title: US-10-664-356-1562

Perfect score: 2130
Sequence: 1 MNPTGLAIFLAVLTVKGL.....YSEKIPSVLFGKIVNPIGK 414

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2130	100.0	414	2	US-09-755-665-14 Sequence 14, Appl
2	2130	100.0	414	2	US-09-755-665-55 Sequence 55, Appl
3	2130	100.0	414	2	US-09-755-665-56 Sequence 56, Appl
4	2130	100.0	415	2	US-09-461-325-134 Sequence 134, App
5	2130	100.0	415	2	US-10-012-542-134 Sequence 134, App
6	2130	100.0	415	2	US-10-115-123-134 Sequence 134, App
7	1798	84.4	351	2	US-09-755-665-57 Sequence 57, Appl
8	842	39.5	377	2	US-10-037-417-66 Sequence 66, Appl
9	798	37.5	394	2	US-08-481-534-6 Sequence 66, Appl
10	792	37.2	394	2	US-08-481-534-11 Sequence 11, Appl
11	791	37.1	394	2	US-08-002-202-6 Sequence 9, Appl
12	790	37.1	394	1	US-08-553-488A-1 Sequence 6, Appl
13	785	36.9	394	2	US-09-755-665-58 Sequence 56, Appl
14	785	36.9	394	2	US-09-023-339-1 Sequence 1, Appl
15	785	36.9	394	1	US-08-121-714-3 Sequence 3, Appl
16	785	36.9	418	1	US-08-477-108A-3 Sequence 3, Appl
17	785	36.9	418	1	US-08-477-112-3 Sequence 3, Appl
18	785	36.9	418	2	US-10-030-330-3 Sequence 3, Appl
19	785	36.9	418	4	PCT-US93-08322-3 Sequence 3, Appl
20	785	36.9	394	1	US-08-002-202-11 Sequence 11, Appl
21	784	36.8	394	1	US-08-002-202-9 Sequence 9, Appl
22	783	36.8	418	2	US-10-000-489-92 Sequence 92, Appl
23	780	36.6	414	2	US-09-518-098B-19 Sequence 19, Appl
24	776	36.4	360	2	US-10-037-417-67 Sequence 17, Appl
25	772.5	36.2	414	1	US-08-002-202-17 Sequence 17, Appl
26	772	36.2	414	2	US-08-481-534-17 Sequence 17, Appl
27	772	36.2	414	1	US-08-481-534-17 Sequence 17, Appl

28	766	36.0	414	1	US-08-002-202-13 Sequence 13, Appl
29	766	36.0	414	2	US-08-481-534-13 Sequence 13, Appl
30	765	35.9	414	1	US-08-002-202-19 Sequence 19, Appl
31	765	35.9	414	2	US-08-481-534-19 Sequence 19, Appl
32	725.5	34.1	414	2	US-09-949-016-8143 Sequence 8143, Ap
33	709.5	33.3	351	2	US-10-000-489-50 Sequence 50, Appl
34	706	33.1	448	2	US-10-104-047-3380 Sequence 3380, Ap
35	703.5	33.0	423	2	US-09-976-594-19 Sequence 19, Appl
36	703.5	33.0	423	2	US-09-919-039-19 Sequence 19, Appl
37	703.5	33.0	435	2	US-09-912-628-5 Sequence 5, Appl
38	701.5	32.9	415	2	US-09-919-039-390 Sequence 390, App
39	698.5	32.8	419	2	US-09-949-016-11541 Sequence 11541, A
40	698	32.8	422	2	US-09-244-111-8 Sequence 8, Appl
41	690.5	32.4	417	2	US-10-012-231A-236 Sequence 236, App
42	690.5	32.4	417	2	US-10-015-389A-236 Sequence 236, App
43	690.5	32.4	417	2	US-10-006-768A-236 Sequence 236, App
44	690.5	32.4	417	2	US-10-015-671A-236 Sequence 236, App
45	690.5	32.4	417	2	US-10-015-393A-236 Sequence 236, App

ALIGNMENTS

```
RESULT 1
US-09-755-665-14
; Sequence 14, Application US/09755665
; Patent No. 660019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumdar, Kumud
; APPLICANT: Tallion, Bruce B.
; APPLICANT: Soderma, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: McDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-755-665-14

Query Match      100.0%; Score 2130; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.7e-197;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MNPTGLAIFLAVLTVKGLKPSFSPRYKALSEVQWQMAAKELARQNDLGFKL 60
Db      1 MNPTGLAIFLAVLTVKGLKPSFSPRYKALSEVQWQMAAKELARQNDLGFKL 60
QY      61 KCAAFNPGNITPLSPISISTAFSMLCLGAQDSTLDEIKGFNFRKMPEDLHGFYII 120
Db      61 KCAAFNPGNITPLSPISISTAFSMLCLGAQDSTLDEIKGFNFRKMPEDLHGFYII 120
QY      121 HELTOKTODKLSIGNTLFDORLOPORKEFLBQAKFYSAETLTITFQNLQMAOKINDF 180
Db      121 HELTOKTODKLSIGNTLFDORLOPORKEFLBQAKFYSAETLTITFQNLQMAOKINDF 180
QY      181 ISQTHGKINLLENIDPQTMLANIYIFPRARKHEFPDNTYKEDPFLKNSSVKVP 240
Db      181 ISQTHGKINLLENIDPQTMLANIYIFPRARKHEFPDNTYKEDPFLKNSSVKVP 240
QY      241 MFRSGIYQGYDQKLSCTTLETPYQNTAIFILPDEGKIKLEKGIQVDTFSRWKTLIS 300
Db      241 MFRSGIYQGYDQKLSCTTLETPYQNTAIFILPDEGKIKLEKGIQVDTFSRWKTLIS 300
QY      301 RRVVDVSVRLHMTGTFTDKKTLISYGVSKIPEHGDLTFKIAPHRSLSKQGEAVHAKELKM 360
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EARLIER APPLICATION NUMBER: 60/090.113
 EARLIER FILING DATE: 1998-06-22
 NUMBER OF SEQ ID NOS: 532
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 134
 LENGTH: 415
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (415)
 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 US-09-461-325-134

Query Match 100.0%; Score 2130; DB 2; Length 415;
 Best Local Similarity 100.0%; Pred. No. 1.7e-197;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVALITVYGLIKPSFSPRNRYKALSEVQGWKQMAKELARQNDLGFRL 60
 DB 1 MNPTGLAIFLAVALITVYGLIKPSFSPRNRYKALSEVQGWKQMAKELARQNDLGFRL 60
 QY 61 KCLAFYNGRNIFLSPISISTAFSMLCLGADSTLDEIKQGFNRKMPKEDLHGFHYII 120
 DB 61 KCLAFYNGRNIFLSPISISTAFSMLCLGADSTLDEIKQGFNRKMPKEDLHGFHYII 120
 QY 121 HELTQKTQDLKLSIGNTLFTDORLQPORKELEDAKNFYSAETILTNFQNLMAQKQINDF 180
 DB 121 HELTQKTQDLKLSIGNTLFTDORLQPORKELEDAKNFYSAETILTNFQNLMAQKQINDF 180
 QY 181 ISQTHGKINNLIENIDPGTVMLANYIFPRARKHEFDPNVTKEDPFLEKNSSVYVPM 240
 DB 181 ISQTHGKINNLIENIDPGTVMLANYIFPRARKHEFDPNVTKEDPFLEKNSSVYVPM 240
 QY 241 MFRSGIYQVGYDDKLSCTIIEIPYQKNITAFILPDEGKIKHLEKGLQVDFSRWKTLLS 300
 DB 241 MFRSGIYQVGYDDKLSCTIIEIPYQKNITAFILPDEGKIKHLEKGLQVDFSRWKTLLS 300
 QY 301 RRVVDVSPRLHMTGTFDLKKTLISYIGVSKI FEEHGLDTIKAPRSLKVGSAVKAELKM 360
 DB 301 RRVVDVSPRLHMTGTFDLKKTLISYIGVSKI FEEHGLDTIKAPRSLKVGSAVKAELKM 360
 QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGIKIVPIGK 414
 DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGIKIVPIGK 414

RESULT 5
 US-10-012-542-134
 Sequence 134, Application US/10012542
 Patent No. 6627741
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: 94 Human Secreted Proteins
 FILE REFERENCE: P2029P1
 CURRENT APPLICATION NUMBER: US/10/012.542
 PRIOR APPLICATION NUMBER: 09/461.325
 PRIOR FILING DATE: 1999-12-14
 PRIOR APPLICATION NUMBER: 60/089.507
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089.508
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089.509
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089.510
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/090.112
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090.113
 PRIOR FILING DATE: 1998-06-22
 NUMBER OF SEQ ID NOS: 532
 SOFTWARE: Patentln Ver. 2.0
 TYPE: PRT

SEQ ID NO 134
 LENGTH: 415
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (415)
 OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
 US-10-012-542-134

Query Match 100.0%; Score 2130; DB 2; Length 415;
 Best Local Similarity 100.0%; Pred. No. 1.7e-197;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVALITVYGLIKPSFSPRNRYKALSEVQGWKQMAKELARQNDLGFRL 60
 DB 1 MNPTGLAIFLAVALITVYGLIKPSFSPRNRYKALSEVQGWKQMAKELARQNDLGFRL 60
 QY 61 KCLAFYNGRNIFLSPISISTAFSMLCLGADSTLDEIKQGFNRKMPKEDLHGFHYII 120
 DB 61 KCLAFYNGRNIFLSPISISTAFSMLCLGADSTLDEIKQGFNRKMPKEDLHGFHYII 120
 QY 121 HELTQKTQDLKLSIGNTLFTDORLQPORKELEDAKNFYSAETILTNFQNLMAQKQINDF 180
 DB 121 HELTQKTQDLKLSIGNTLFTDORLQPORKELEDAKNFYSAETILTNFQNLMAQKQINDF 180
 QY 181 ISQTHGKINNLIENIDPGTVMLANYIFPRARKHEFDPNVTKEDPFLEKNSSVYVPM 240
 DB 181 ISQTHGKINNLIENIDPGTVMLANYIFPRARKHEFDPNVTKEDPFLEKNSSVYVPM 240
 QY 241 MFRSGIYQVGYDDKLSCTIIEIPYQKNITAFILPDEGKIKHLEKGLQVDFSRWKTLLS 300
 DB 241 MFRSGIYQVGYDDKLSCTIIEIPYQKNITAFILPDEGKIKHLEKGLQVDFSRWKTLLS 300
 QY 301 RRVVDVSPRLHMTGTFDLKKTLISYIGVSKI FEEHGLDTIKAPRSLKVGSAVKAELKM 360
 DB 301 RRVVDVSPRLHMTGTFDLKKTLISYIGVSKI FEEHGLDTIKAPRSLKVGSAVKAELKM 360
 QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGIKIVPIGK 414
 DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGIKIVPIGK 414

RESULT 6
 US-10-115-123-134
 Sequence 134, Application US/10115123
 Patent No. 6774216
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: 94 Human Secreted Proteins
 FILE REFERENCE: P2029G30AFID2
 CURRENT APPLICATION NUMBER: US/10/115.123
 CURRENT FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: PCT/US99/13418
 PRIOR FILING DATE: 1999-06-15
 PRIOR APPLICATION NUMBER: 60/089.507
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089.508
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089.509
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089.510
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/090.112
 PRIOR FILING DATE: 1998-06-22
 PRIOR APPLICATION NUMBER: 60/090.113
 PRIOR FILING DATE: 1998-06-22
 NUMBER OF SEQ ID NOS: 532
 SOFTWARE: Patentln Ver. 2.0
 SEQ ID NO 134
 LENGTH: 415
 TYPE: PRT

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (415)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-115-123-134

Query Match 100.0%; Score 2130; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.7e-197;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPFLGLATLVALLTYKGLKPSFSPRNKALSEVCGKQKMAKELAQNDLGFKL 60
DB 1 MNPFLGLATLVALLTYKGLKPSFSPRNKALSEVCGKQKMAKELAQNDLGFKL 60
QY 61 KKLAFFNPGNIFLSPSTAFSMCLGAQDSTLDEIKQGFNRKPEKDLHGFFYII 120
DB 61 KKLAFFNPGNIFLSPSTAFSMCLGAQDSTLDEIKQGFNRKPEKDLHGFFYII 120
QY 121 HELTQKTDKLSIGNTLFIQRLQPKRFLDANKFYSAETLLTNFQNLMAQKQINDF 180
DB 121 HELTQKTDKLSIGNTLFIQRLQPKRFLDANKFYSAETLLTNFQNLMAQKQINDF 180
QY 181 ISQKTKGKINNLEINIDPGTWMLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVP 240
DB 181 ISQKTKGKINNLEINIDPGTWMLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVP 240
QY 241 MPFSGIYQVGYDDKLSCTTLEIPYOKNITAFILPDEGKLKLEKGLQVDTFSRMKTLIS 300
DB 241 MPFSGIYQVGYDDKLSCTTLEIPYOKNITAFILPDEGKLKLEKGLQVDTFSRMKTLIS 300
QY 301 RRVVDVSVPLHMTGTFDLKKTLSYIGVSKIFEEHGDLTAKIAPHRSLSKVGAEVHKELKM 360
DB 301 RRVVDVSVPLHMTGTFDLKKTLSYIGVSKIFEEHGDLTAKIAPHRSLSKVGAEVHKELKM 360
QY 361 DERGTGAAGTGAGTQTPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414
DB 361 DERGTGAAGTGAGTQTPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414

RESULT 7

US-09-755-665-57
Sequence 57, Application US/09755665
Patent No. 6600019
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tailon, Bruce E.
APPLICANT: Spaderma, Steven K.
APPLICANT: Spytek, Kimberly A.
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
LENGTH: 361
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)..(361)
OTHER INFORMATION: wherein Xaa is any amino acid as defined in the
OTHER INFORMATION: specification
US-09-755-665-57

Query Match 84.4%; Score 1798; DB 2; Length 361;
Best Local Similarity 96.7%; Pred. No. 1.9e-165;
Matches 349; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 54 DLGFKLLKQLAFNPGNIFLSPSTAFSMCLGAQDSTLDEIKQGFNRKPEKDLH 113
DB 1 DLGFKLLKQLAFNPGNIFLSPSTAFSMCLGAQDSTLDEIKQGFNRKPEKDLH 60
QY 114 EGFHYIIHELTQKTDKLSIGNTLFIQRLQPKRFLDANKFYSAETLLTNFQNLMA 173
DB 61 EGFHYIIHELTQKTDKLSIGNTLFIQRLQPKRFLDANKFYSAETLLTNFQNLMA 120
QY 174 QKQINDFISQKTKGKINNLEINIDPGTWMLANYIFPRARKHEPDNVTKEEDFLEK 233
DB 121 QKQINDFISQKTKGKINNLEINIDPGTWMLANYIFPRARKHEPDNVTKEEDFLEK 180
QY 234 SSVKVPMMFSGIYQVGYDDKLSCTTLEIPYOKNITAFILPDEGKLKLEKGLQVDTFS 293
DB 181 SSVKVPMMFSGIYQVGYDDKLSCTTLEIPYOKNITAFILPDEGKLKLEKGLQVDTFS 240
QY 294 RMTLLSRVVDVSVPLHMTGTFDLKKTLSYIGVSKIFEEHGDLTAKIAPHRSLSKVGAEV 353
DB 241 RMTLLSRVVDVSVPLHMTGTFDLKKTLSYIGVSKIFEEHGDLTAKIAPHRSLSKVGAEV 300
QY 354 HRAELKMDERGBGAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIG 413
DB 301 HRAELKMDERBXXXXXXXLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIG 360
QY 414 K 414
DB 361 K 361

RESULT 8

US-10-037-417-66
Sequence 66, Application US/10037417
Patent No. 6903201
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Paturajan, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine B
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Eilerman, Karen
APPLICANT: Malyskar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David M
APPLICANT: Padigaru, Muralidhara
APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles B
APPLICANT: Eissen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02

Query Match	39.5%;	Score 842;	DB 2;	Length 377;
Best Local Similarity	43.7%;	Pred. No. 6.6e-73;		
Matches 163;	Conservative 86;	Mismatches 118;	Indels 6;	Gaps 4;

RESULT 9
US-08-481-534-6
; Sequence 6, Application US/08481534

STATE: IL

Query Match 37.5%; Score 798; DB 2; Length 394;
Best Local Similarity 43.3%; Pred. NO. 1.3e-68;
Matches 157; Conservative 72; Mismatches 132; Indels 2; Gaps 1.

Db 392 Tgk 394

TITLE OF INVENTION: Endoprotease

```

/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
/ STREET: 300 South Wacker Drive
/ CITY: Chicago
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/481,534
/ FILING DATE: 14-SEP-1995
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6022855nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 92,448-D
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-913-0001
/ TELEFAX: 312-913-0002
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 394 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Modified site
/ LOCATION: 355..358
/ OTHER INFORMATION: /label=Variant
/ OTHER INFORMATION: /note="The amino acid sequence is the amino acid
/ OTHER INFORMATION: sequence of the modified alpha-1-antitrypsin
/ OTHER INFORMATION: protein, alpha-1-antitrypsin Pittsburgh."
US-08-481-534-11

Query Match 37.2%; Score 792; DB 2; Length 394;
Best Local Similarity 43.0%; Pred. No. 4.8e-68;
Matches 156; Conservative 72; Mismatches 133; Indels 2; Gaps 1;

QY 54 DLGFKLLKLAAYNPGRNIFLSPISITAFSMCLGAQSDTDEIRKGFNR--KAPKED 111
DB 32 EFAPSLYRQLAHQSNSTNIFSPVSIAITAFAMLSGTAKADTHDELGLNFNLTQIPBAQ 91
QY 112 LHGFGHYITHELTOQTODKLSTIGNTLFDQRLQPORKFLBDANKFYSAETIITFONLE 171
DB 92 IHGFGQELLRLTNQDPDQQLTNGGLFLSQGLKLVDFKFLBDVKKLYHSEAFVNFGDTE 151
QY 172 MAQKOINDFISQTHGKINNLINIDPGTWMLANYIFPRARKHEPDNVTKEEDFFLE 231
DB 152 QAKKOINDVEKGTQKIVDLVKELDRTVPALVNTIFFKGMKRPFEVYDEEDFHYD 211
QY 232 KNSSVVPMMPFRSGIYQVGYDDKLSCTIIEIPYOKNITAIFILPDEGKLGKLEKGLQVDT 291
DB 212 QYTVKVPWPKLGMFNIGHCCKLSSWVLMKYLGNATAIFFLPDGGKLOHLENELTHDI 271
QY 292 FSRWKTLISRVDVSVPRLMATGTDTLKKTLSTYGVSKIFEEHGGULTIAPHRSLKVEE 351
DB 272 IYKFLNENEDRSASLHLPGLSTIGTYDLKSVGLQGLITKVFSGADLSGTEBAPLKLK 331
QY 352 AVHKAELKMDERGTEGAAGTGAQTLPMENPLVYKIDKPYILLIYSKISVFLGIQVNP 411
DB 332 AHKAVLITIDEGTEBAAGMPLAIPRSIPPEVKENKPFVLMIEONTSPLEPMGKVNBP 391
QY 412 IGG 414
DB 392 TGG 394
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RESULT 11
US-08-481-534-9
/ Sequence 9; Application US/08481534
/ Patent No. 6022855
/ GENERAL INFORMATION:
/ APPLICANT: Thomas, Gary
/ APPLICANT: Anderson, Eric D
/ APPLICANT: Thomas, Laurel
/ APPLICANT: Hayflick, Joel S
/ APPLICANT: Nelson, Jay
/ APPLICANT: Stenglen, Stephan G
/ TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
/ STREET: 300 South Wacker Drive
/ CITY: Chicago
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/481,534
/ FILING DATE: 14-SEP-1995
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6022855nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 92,448-D
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-913-0001
/ TELEFAX: 312-913-0002
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 394 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ FEATURE:
/ NAME/KEY: Modified site
/ LOCATION: 355..358
/ OTHER INFORMATION: /label=Variant
/ OTHER INFORMATION: /note="The amino acid sequence is the amino acid
/ OTHER INFORMATION: sequence of the modified alpha-1-antitrypsin
/ OTHER INFORMATION: protein, alpha-1-antitrypsin Portland."
US-08-481-534-9

Query Match 37.1%; Score 791; DB 2; Length 394;
Best Local Similarity 43.0%; Pred. No. 6e-68;
Matches 156; Conservative 72; Mismatches 133; Indels 2; Gaps 1;

QY 54 DLGFKLLKLAAYNPGRNIFLSPISITAFSMCLGAQSDTDEIRKGFNR--KAPKED 111
DB 32 EFAPSLYRQLAHQSNSTNIFSPVSIAITAFAMLSGTAKADTHDELGLNFNLTQIPBAQ 91
QY 112 LHGFGHYITHELTOQTODKLSTIGNTLFDQRLQPORKFLBDANKFYSAETIITFONLE 171
DB 92 IHGFGQELLRLTNQDPDQQLTNGGLFLSQGLKLVDFKFLBDVKKLYHSEAFVNFGDTE 151
QY 172 MAQKOINDFISQTHGKINNLINIDPGTWMLANYIFPRARKHEPDNVTKEEDFFLE 231
DB 152 QAKKOINDVEKGTQKIVDLVKELDRTVPALVNTIFFKGMKRPFEVYDEEDFHYD 211
QY 212 QYTVKVPWPKLGMFNIGHCCKLSSWVLMKYLGNATAIFFLPDGGKLOHLENELTHDI 271
DB 272 IYKFLNENEDRSASLHLPGLSTIGTYDLKSVGLQGLITKVFSGADLSGTEBAPLKLK 331
QY 332 AVHKAELKMDERGTEGAAGTGAQTLPMENPLVYKIDKPYILLIYSKISVFLGIQVNP 411
DB 392 TGG 394
```

QY 292 PSNRKTLISRRVVDVSPRLMTGTDFDLKTLISYIGVSKIPEEHGDLTKIAPHRSKLVGE 351
Db 272 IYKLEBNDRRSASLH.PKLSITGTVDLKSVLGQLGITKVFNSCADLSGVTBEAPLTKSK 331
QY 352 AVHKAELKMDERBEGAGAGTOLPMETPLVYKIDKPYLLIYSEKIPSVLFLGKIVNP 411
Db 332 AVHKAVALTIDKGTBAAGAMFLERIPRSIPPEVKNKPFVFLMIKONTKSPLEFGKIVNP 391
QY 412 ICK 414
Db 392 TCK 394

RESULT 12

US-08-002-202-6
; Sequence 6, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Garry
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Furin Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti and Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,202
; FILING DATE: 08-JAN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5604201nan, Kevin E
; REGISTRATION NUMBER: 35,30003
; REFERENCE/DOCKET NUMBER: 92,448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-002-202-6

Query Match 37.1%; Score 790; DB 1; Length 394;

Best Local Similarity 43.0%; Pred. No. 7,5e-68;
Matches 156; Conservative 72; Mismatches 133; Indels 2; Gaps 1;

QY 54 DLGFKLLKLAFAFNPGNITPLSISTAPSMCLGADSTLDEIKGFMFR--KMPKED 111
Db 32 BPAFSLYKQLAHGNSNITPSPVSIATAPAMSLGKADTDBILGILNPNLTETPEAQ 91
QY 112 LHGEFYIITHELTOXTDLKLSIGNTLFIQRLQPKRKPLEDAKNFYSAETIILNPNLE 171
Db 92 IHGFGELIATLWQPSQLTLTGNGFLSGQLKLVDKFLBVDYKLYHSAFVYNPQDTE 151
QY 172 MAOKQINDPISQTHGKINNLINIDPGTLMLANIYFPFAKMGHEPDVNTYKEDFLB 231
Db 152 QAKKQINDVYKGTGKIYDLVYKELDRDTVPALVNIYFPGKWBKRPPEVVDTESEDPHVD 211

QY 232 KNSVVKVPMFRSGIYGVYDDKLSCTILIEIPYOKNTAIFILPDEBGLKRLKGLQVDT 291
Db 212 QVTTVAVPMKRLGFMPIQCKKLSWVLMKTLGNATLFFLPDEBGLQHLNELTHDI 271
QY 292 PSNRKTLISRRVVDVSPRLMTGTDFDLKTLISYIGVSKIPEEHGDLTKIAPHRSKLVGE 351
Db 272 IYKLEBNDRRSASLH.PKLSITGTVDLKSVLGQLGITKVFNSCADLSGVTBEAPLTKSK 331
QY 352 AVHKAELKMDERBEGAGAGTOLPMETPLVYKIDKPYLLIYSEKIPSVLFLGKIVNP 411
Db 332 AVHKAVALTIDKGTBAAGAMFLERIPRSIPPEVKNKPFVFLMIKONTKSPLEFGKIVNP 391
QY 412 ICK 414
Db 392 TCK 394

RESULT 13

US-08-553-488A-1
; Sequence 1, Application US/08553488A
; Patent No. 5817484
; GENERAL INFORMATION:
; APPLICANT: YU, Myeong-Hee
; APPLICANT: KWON, Ki-Sun
; APPLICANT: LEE, Kee-Nyung
; APPLICANT: SHIN, Hwa-Soo
; TITLE OF INVENTION: THERMORESISTANT ALPHA-1-ANTITRYPSIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YU, Myeong-Hee
; STREET: 3-1003, Hankang Apartment, 49-8, Jamwon-dong,
; STREET: Secho-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 137-030
; ADDRESSEE: KWON, Ki-Sun
; STREET: 130-1306, Hanbit Apartment, Oun-dong,
; STREET: Yuseong-gu
; CITY: Taejeon
; STATE: Taejeon
; COUNTRY: Republic of Korea
; ZIP: 305-333
; ADDRESSEE: SHIN, Hwa-Soo
; STREET: 3-303, Sindonga Apartment, Yongjeon-dong,
; STREET: Dong-gu
; CITY: Taejeon
; STATE: Taejeon
; COUNTRY: Republic of Korea
; ZIP: 300-200
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,488A
; FILING DATE: 20-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 93-8510
; FILING DATE: 18-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
OTHER INFORMATION: wild type human '-1-antitrypsin
US-08-553-488A-1

Query Match 37.1%; Score 790; DB 1; Length 394;

Best Local Similarity 42.7%; Pred. No. 7,5e-68;
Matches 155; Conservative 74; Mismatches 132; Indels 2; Gaps 1;

QY 54 DLGFKLLKLAAPNPGNITFLSPISISTAFSMCLGAQDSTLDEIKOGFNR--KMEKD 111
DB 32 EFAPSLYRQLAHOSNSTNIFSPVSITATAPAMLSVGTAKDTHDEILGELNFTLEIPQA 91
QY 112 LHGFPYIHELTOQTODKLSIGNTLFIDORLOPQKPLEDAKNFYSAETILTNPONLE 171
DB 92 IHGFOELRLTKLPDSQQLTGTGNGLFLSEGLKLVDPKLEVDKLVHSAFTVNFQDTE 151
QY 172 MAQKQINDFISQTHGKINNLINIDPGYMLLANTYIFFRARKHEFDPNVTKEDPFLE 231
DB 152 EAKKQINNVEKKTQCKVVDLVKELDRDVFALVNIYFFKQWERPFEVATEEEDFHYD 211
QY 232 KNSVVPVPMFRSGIYQVGDLSCTTLEIPYQKNTAIFLLPDSGKLKHEKGQVDT 291
DB 212 QATTVVPMRRKLGMPNICHCKLSWVLMKYLGNATAIFFLPDSGKLQHLNELTHDI 271
QY 292 FSRWKTLLSRVVDVSPRLHMTGTPDLKKTLSYIGVSKI FEEHGDLTAKIAPHRSIKVG 351
DB 272 ITKFLNENRRSANHLPRKLAITGTVDLTKVIGHLGTIVFSGADLSGVTEDAPLKSK 330
QY 352 AVHKAELKDERGTEGAAGTACTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYVP 411
DB 332 AVHKAULTIDEKTEAAGAMFLAIPMSIPPEVKFKPFFVLMIEQNTKSPLEFGKYNP 360
QY 412 IGR 414
DB 392 TQK 394

RESULT 14

US-09-755-665-58
Sequence 58, Application US/09755665
Patent No. 6600019
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tailion, Bruce E.
APPLICANT: Spaderma, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755, 665
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
LENGTH: 363
TYPE: PRP
ORGANISM: Homo sapiens
US-09-755-665-58

Query Match 36.9%; Score 785; DB 2; Length 363;

Best Local Similarity 41.6%; Pred. No. 2e-67;
Matches 151; Conservative 83; Mismatches 127; Indels 2; Gaps 1;

QY 54 DLGFKLLKLAAPNPGNITFLSPISISTAFSMCLGAQDSTLDEIKOGFNR--KMEKD 111
DB 1 EFAPSLYRQLAHOSNSTNIFSPVSITATAPAMLSVGTAKDTHDEILGELNFTLEIPQA 60
QY 112 LHGFPYIHELTOQTODKLSIGNTLFIDORLOPQKPLEDAKNFYSAETILTNPONLE 171
DB 61 IHGFOELRLTKLPDSQQLTGTGNGLFLSEGLKLVDPKLEVDKLVHSAFTVNFQDTE 120
QY 172 MAQKQINDFISQTHGKINNLINIDPGYMLLANTYIFFRARKHEFDPNVTKEDPFLE 231
DB 121 EAKKQINNVEKKTQCKVVDLVKELDRDVFALVNIYFFKQWERPFEVATEEEDFHYD 180
QY 232 KNSVVPVPMFRSGIYQVGDLSCTTLEIPYQKNTAIFLLPDSGKLKHEKGQVDT 291
DB 181 QATTVVPMRRKLGMPNICHCKLSWVLMKYLGNATAIFFLPDSGKLQHLNELTHDI 240
QY 292 FSRWKTLLSRVVDVSPRLHMTGTPDLKKTLSYIGVSKI FEEHGDLTAKIAPHRSIKVG 351
DB 241 ITKFLNENRRSANHLPRKLAITGTVDLTKVIGHLGTIVFSGADLSGVTEDAPLKSK 300
QY 352 AVHKAELKDERGTEGAAGTACTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYVP 411
DB 301 AVHKAULTIDEKTEAAGAMFLAIPMSIPPEVKFKPFFVLMIEQNTKSPLEFGKYNP 360
QY 412 IGR 414
DB 361 TQK 363

RESULT 15

US-09-023-339-1
Sequence 1, Application US/09023339
Patent No. 6127145
GENERAL INFORMATION:
APPLICANT: Sulliff, Thomas D.
APPLICANT: Rodriguez, Raymond L.
TITLE OF INVENTION: Production of '-1-Antitrypsin
TITLE OF INVENTION: in Plants
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,339
FILING DATE: 13-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,991
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Pelichory, Joanne R
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 0665-0003.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

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Db 301 RRVVSVSPRLHMTGTFDLKTSLTSTYGVSKIFEHGDLTAKIAPHSLKGVAAHAKALKM 360
 Qy 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLGKI VNPIGK 414
 Db 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLGKI VNPIGK 414

RESULT 2
 US-09-755-665-55

Sequence 55, Application US/09755665
 Patent No. 6600019
 GENERAL INFORMATION:
 APPLICANT: Prayaga, Sudhidas K.
 APPLICANT: Majumder, K. K.
 APPLICANT: Tailon, Bruce E.
 APPLICANT: Spaderna, Steven K.
 APPLICANT: Spytek, Kimberly A.
 APPLICANT: MacDougall, John
 TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
 FILE REFERENCE: 15966-631
 CURRENT APPLICATION NUMBER: US/09/755,665
 CURRENT FILING DATE: 2001-08-14
 PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
 PRIOR FILING DATE: 2000-01-06
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 55
 LENGTH: 414
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-755-665-55

*NOVX polypeptides
 re productive
 abnormal males
 endocrinological defects
 pathologic spermatogenesis*

Query Match 100.0%; Score 2130; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 1,7e-197;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPTGLAIFLAVALITVKGILKPSFSPRNRYKALSEVQGMKORMAKELARQNDLGFKLL 60
 Db 1 MNPTGLAIFLAVALITVKGILKPSFSPRNRYKALSEVQGMKORMAKELARQNDLGFKLL 60
 Qy 61 KCLAFYNGRNIPLSPISISTAFSMLCLGAODSTLDEIKGFNFRKMPBEKDLHGFHYII 120
 Db 61 KCLAFYNGRNIPLSPISISTAFSMLCLGAODSTLDEIKGFNFRKMPBEKDLHGFHYII 120
 Qy 121 HELTQKODKLSTIGNTLFIIDRLQOPORKEFLDANKFYSAETILTNPONLEMAOKQINDF 180
 Db 121 HELTQKODKLSTIGNTLFIIDRLQOPORKEFLDANKFYSAETILTNPONLEMAOKQINDF 180
 Qy 121 ISQTHGKINLLIENIDPGTVMLLANYIFPRARWKEHFDNVTKEEDFLEKNSSVKVP 240
 Db 121 ISQTHGKINLLIENIDPGTVMLLANYIFPRARWKEHFDNVTKEEDFLEKNSSVKVP 240
 Qy 181 ISQTHGKINLLIENIDPGTVMLLANYIFPRARWKEHFDNVTKEEDFLEKNSSVKVP 240
 Db 181 ISQTHGKINLLIENIDPGTVMLLANYIFPRARWKEHFDNVTKEEDFLEKNSSVKVP 240
 Qy 241 MFRSGIYGVGDDKSLTILIEIPYOKNITAFILPDGSKLHLEKGLQVDFFSWKTLIS 300
 Db 241 MFRSGIYGVGDDKSLTILIEIPYOKNITAFILPDGSKLHLEKGLQVDFFSWKTLIS 300
 Qy 301 RRVVSVSPRLHMTGTFDLKTSLTSTYGVSKIFEHGDLTAKIAPHSLKGVAAHAKALKM 360
 Db 301 RRVVSVSPRLHMTGTFDLKTSLTSTYGVSKIFEHGDLTAKIAPHSLKGVAAHAKALKM 360
 Qy 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLGKI VNPIGK 414
 Db 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLGKI VNPIGK 414

RESULT 3
 US-09-755-665-56
 Sequence 56, Application US/09755665
 Patent No. 6600019
 GENERAL INFORMATION:
 APPLICANT: Prayaga, Sudhidas K.
 APPLICANT: Majumder, K. K.

APPLICANT: Tailon, Bruce E.
 APPLICANT: Spaderna, Steven K.
 APPLICANT: Spytek, Kimberly A.
 APPLICANT: MacDougall, John
 TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
 FILE REFERENCE: 15966-631
 CURRENT APPLICATION NUMBER: US/09/755,665
 CURRENT FILING DATE: 2001-08-14
 PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
 PRIOR FILING DATE: 2000-01-06
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 56
 LENGTH: 414
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-755-665-56

Query Match 100.0%; Score 2130; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 1,7e-197;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPTGLAIFLAVALITVKGILKPSFSPRNRYKALSEVQGMKORMAKELARQNDLGFKLL 60
 Db 1 MNPTGLAIFLAVALITVKGILKPSFSPRNRYKALSEVQGMKORMAKELARQNDLGFKLL 60
 Qy 61 KCLAFYNGRNIPLSPISISTAFSMLCLGAODSTLDEIKGFNFRKMPBEKDLHGFHYII 120
 Db 61 KCLAFYNGRNIPLSPISISTAFSMLCLGAODSTLDEIKGFNFRKMPBEKDLHGFHYII 120
 Qy 121 HELTQKODKLSTIGNTLFIIDRLQOPORKEFLDANKFYSAETILTNPONLEMAOKQINDF 180
 Db 121 HELTQKODKLSTIGNTLFIIDRLQOPORKEFLDANKFYSAETILTNPONLEMAOKQINDF 180
 Qy 121 ISQTHGKINLLIENIDPGTVMLLANYIFPRARWKEHFDNVTKEEDFLEKNSSVKVP 240
 Db 121 ISQTHGKINLLIENIDPGTVMLLANYIFPRARWKEHFDNVTKEEDFLEKNSSVKVP 240
 Qy 181 ISQTHGKINLLIENIDPGTVMLLANYIFPRARWKEHFDNVTKEEDFLEKNSSVKVP 240
 Db 181 ISQTHGKINLLIENIDPGTVMLLANYIFPRARWKEHFDNVTKEEDFLEKNSSVKVP 240
 Qy 241 MFRSGIYGVGDDKSLTILIEIPYOKNITAFILPDGSKLHLEKGLQVDFFSWKTLIS 300
 Db 241 MFRSGIYGVGDDKSLTILIEIPYOKNITAFILPDGSKLHLEKGLQVDFFSWKTLIS 300
 Qy 301 RRVVSVSPRLHMTGTFDLKTSLTSTYGVSKIFEHGDLTAKIAPHSLKGVAAHAKALKM 360
 Db 301 RRVVSVSPRLHMTGTFDLKTSLTSTYGVSKIFEHGDLTAKIAPHSLKGVAAHAKALKM 360
 Qy 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLGKI VNPIGK 414
 Db 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLGKI VNPIGK 414

RESULT 4
 US-09-461-325-134
 Sequence 134, Application US/09461325A
 Patent No. 6475753
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: 94 Human Secreted Proteins
 FILE REFERENCE: P2029P1
 CURRENT APPLICATION NUMBER: US/09/461,325A
 CURRENT FILING DATE: 1999-12-14
 EARLIER APPLICATION NUMBER: PCT/US99/13418
 EARLIER FILING DATE: 1999-06-15
 EARLIER APPLICATION NUMBER: 60/089,507
 EARLIER FILING DATE: 1998-06-16
 EARLIER APPLICATION NUMBER: 60/089,508
 EARLIER FILING DATE: 1998-06-16
 EARLIER APPLICATION NUMBER: 60/089,509
 EARLIER FILING DATE: 1998-06-16
 EARLIER APPLICATION NUMBER: 60/089,510
 EARLIER FILING DATE: 1998-06-16
 EARLIER APPLICATION NUMBER: 60/090,112
 EARLIER FILING DATE: 1998-06-22

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 31, 2006, 09:41:45 ; Search time 188 Seconds
(without alignments)
967.568 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 2130
Sequence: 1 MNPTLGIAFLAVLTWKGL.....YSEKIPSVLFGKIVNPIGK 414

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A_Geneseq_21.*
1: geneseqp1980s.*
2: geneseqp1980s.*
3: geneseqp2000s.*
4: geneseqp2000s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2130	100.0	414	AAU05754	Aa05754 Human NOV
2	2130	100.0	414	AAE04885	Aae04885 Human pro
3	2130	100.0	414	ADA57300	Ada57300 Human sec
4	2130	100.0	414	ADA41179	Ada41179 Human sec
5	2130	100.0	414	ADN05952	Adn05952 Antipepti
6	2130	100.0	415	AAV86217	Aav86217 Human sec
7	2130	100.0	415	ABO53360	Ab053360 Novel hum
8	2130	99.7	414	AAW78898	Aaw78898 Human pro
9	2114	99.2	431	ABBI1832	Abbi1832 Human sec
10	2114	99.2	431	AAW78882	Aaw78882 Human pro
11	1783	83.7	358	AAU05759	Aau05759 Human NOV
12	795	37.3	348	AAU05877	Aau05877 Sequence
13	792	37.2	394	AAV44205	Aav44205 Alpha-1 a
14	791	37.1	394	AAV44201	Aav44201 Alpha-1 a
15	791	37.1	418	AAK22931	Aak22931 Alpha-1 a
16	790	37.1	394	AAK67363	Aak67363 Human alp
17	790	37.1	394	AAK67360	Aak67360 Human alp
18	787	36.9	418	AAAP5021	Aap5021 Sequence
19	786	36.9	394	AAK67362	Aak67362 Alpha-1 a
20	785	36.9	418	ADBE6631	Adbe6631 Human pro
21	785	36.9	418	ADDA5920	Adda5920 Human pro
22	786	36.9	418	ADK70484	Adk70484 Respirato
23	786	36.9	418	ADQ39557	Adq39557 Human myo
24	786	36.9	418	ADQ39553	Adq39553 Human myo

25	786	36.9	418	ADQ39558	Adq39558 Human myo
26	786	36.9	418	ADQ39559	Adq39559 Human myo
27	786	36.9	418	ADQ39555	Adq39555 Human myo
28	786	36.9	418	ADQ39556	Adq39556 Human myo
29	786	36.9	418	ADQ39554	Adq39554 Human myo
30	785.5	36.9	413	ADF28926	Adf28926 Rabbit al
31	785	36.9	394	AAW59839	Aaw59839 Mature pr
32	785	36.9	394	AAU59873	Aau59873 Human alp
33	785	36.9	394	ADA26998	Ada26998 Human alp
34	785	36.9	395	ADX59020	Adx59020 Human alp
35	785	36.9	398	ADM82878	Adm82878 Mouse alp
36	785	36.9	411	ADBE3530	Adbe3530 Rat Prote
37	785	36.9	411	ADBE3526	Adbe3526 Rat Prote
38	785	36.9	411	ADBE3522	Adbe3522 Rat Prote
39	785	36.9	411	ADBE3534	Adbe3534 Rat Prote
40	785	36.9	411	ADDA5919	Adda5919 Rat Prote
41	785	36.9	411	ADBE0629	Adbe0629 Rat Prote
42	785	36.9	418	AAAP40133	Aap40133 Sequence
43	785	36.9	418	AAAP4664	Aap4664 Predomina
44	785	36.9	418	AAV26925	Aav26925 Human alp
45	785	36.9	418	ABG96414	Abg96414 Human ova

ALIGNMENTS

RESULT 1	AAU05754	AAU05754 standard; protein; 414 AA.
ID	AAU05754	
AC	AAU05754	
XX	24-OCT-2001	(first entry)
DT	24-OCT-2001	
XX	Human NOV7 polypeptide.	
DE	Human NOV7 polypeptide.	
XX	Human, NOV7; AL132990 B; fertility disorder; spermatogenesis; cardiac; cytoesatic; immunomodulatory; antiproliferative; antidiabetic;	
KW	cell proliferation; cancer; diabetic retinopathy; angiogenic disorder;	
KW	pulmonary disorder; hematopoietic disorder; immunological disorder;	
KW	inflammatory disorder; tumour related disorders; emphysema; cirrhosis;	
KW	wound healing; gene therapy.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200149729-A2.	
XX		
PD	12-JUL-2001.	
XX		
PF	05-JAN-2001; 2001MO-US000299.	
XX		
PR	06-JAN-2000; 2000US-0174724P.	
PR	11-JAN-2000; 2000US-0175434P.	
PR	11-JAN-2000; 2000US-0175488P.	
PR	12-JAN-2000; 2000US-0175596P.	
PR	12-JAN-2000; 2000US-0175743P.	
PR	13-JAN-2000; 2000US-0175819P.	
PR	07-AUG-2000; 2000US-0223524P.	
PR	04-JAN-2001; 2001US-00755665.	
PA	(CURA-) CURAGEN CORP.	
XX		
PI	Prayaga SK, Majumder K, Tallon BF, Spaderma SK, Spytek KA, Macdonald J,	
XX		
DR	WPI; 2001-418356/44.	
DR	N-PSDB; AAS10874.	
XX		
PT	Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful for treating a syndrome associated with a NOVX-associated disorder, e.g. cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or pulmonary disorder.	
PT		
XX		

PS Claim 1, Page 32, 144pp; English.

XX The invention relates to nucleic acids encoding NOVX (X being an integer
 CC from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
 CC useful in diagnosing, treating or manufacturing a medicament for a
 CC disease or disorder associated with NOVX e.g. cell proliferation (cancer
 CC and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
 CC disorders (e.g. of spermatogenesis), haematopoietic, immunological,
 CC inflammatory and tumour related disorders, emphysema, cirrhosis, wound
 CC healing. NOVX nucleic acids are also useful in gene therapy. They are
 CC also used for screening for a modulator of activity or of latency or
 CC predisposition to a NOVX-associated disorder. They are also useful for
 CC determining the presence of or predisposition to a NOVX-associated
 CC disorder. The present sequence represents NOV7 (Al132990 B), which has
 CC sequence homology to an unidentified human secreted protein (HWHGUS54)
 CC and to alpha anti-trypsin

XX Sequence 414 AA;

SO

Query Match 100.0%; Score 2130; DB 4; Length 414;
 Best Local Similarity 100.0%; Pred. No. 4.4e-181;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVLITLVKGLKPSFSPRYKALSEVQGMKORMAAKELARQNDLGFKLL 60
 DB 1 MNPTGLAIFLAVLITLVKGLKPSFSPRYKALSEVQGMKORMAAKELARQNDLGFKLL 60

QY 61 KKLAFNPGRNIFLPLSISTAFSMLCIGAQDSTLDEIKOGFNPFRKPEKDLHEGFHYII 120
 DB 61 KKLAFNPGRNIFLPLSISTAFSMLCIGAQDSTLDEIKOGFNPFRKPEKDLHEGFHYII 120

QY 121 HELTQKTQDLKLSIGNTLFIIDRLQPKRFLBDANKFYSAEITLITNFOULEMAQKQINDP 180
 DB 121 HELTQKTQDLKLSIGNTLFIIDRLQPKRFLBDANKFYSAEITLITNFOULEMAQKQINDP 180

QY 181 ISQKTHGKINNIENIDPGTVMLANVIFPRARWKHEPDNVTKEEFLFKNSSSVKVPV 240
 DB 181 ISQKTHGKINNIENIDPGTVMLANVIFPRARWKHEPDNVTKEEFLFKNSSSVKVPV 240

QY 241 MFRSGIYGVGYDDKLSCTTLEIPIYQKNITAIFILPDEGKHLKELKQVDTFSRWKTLIS 300
 DB 241 MFRSGIYGVGYDDKLSCTTLEIPIYQKNITAIFILPDEGKHLKELKQVDTFSRWKTLIS 300

QY 301 RRVADVSVPLRMTGTFDLKKTLISYIGVSKIPEHGDLTAKIAPHSLSIKVGEAVHKAELKX 360
 DB 301 RRVADVSVPLRMTGTFDLKKTLISYIGVSKIPEHGDLTAKIAPHSLSIKVGEAVHKAELKX 360

QY 361 DERGTGAGCTGAGTIPMETPLVVKIDKPYLLIYSEKIPSVPLFKGIYVPIGK 414
 DB 361 DERGTGAGCTGAGTIPMETPLVVKIDKPYLLIYSEKIPSVPLFKGIYVPIGK 414

RESULT 2
 AAE04885
 ID AAE04885 standard; protein; 414 AA.
 XX
 AC AAE04885;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Human protease protein-12 (PRTS-12).
 XX
 XX Human; protease protein-12; PRTS-12; cytostatic; hypotensive; antiviral;
 KW gastrointestinal disorder; anorexia; dysphagia; cardiovascular disorder;
 KW atherosclerosis; vasculitis; autoimmune disorder; inflammatory disorder;
 KW Alzheimer's disease; cell proliferative disorder; dermatitis; cirrhosis;
 KW acquired immune deficiency syndrome; AIDS; neurological disorder; asthma;
 KW developmental disorder; epithelial disorder; eczema; dementia; noctropic;
 KW neurological disorder; reproductive disorder; infertility; teratogenesis;
 KW immunosuppressive; drug screening; actinic keratosis; cardiac; epilepsy;
 KW anaemia; anticancer; gene therapy; antibacterial.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..19
 FT Peptide /label= Signal_peptide
 FT Protein 20..414
 FT /note= "Mature human PRTS-12"

XX MO200146443-A2.
 XX
 XX 28-JUN-2001.
 XX
 XX 19-DEC-2000; 2000MO-US034811.
 XX
 XX 23-DEC-1999; 99US-0172055P.
 XX 21-JAN-2000; 2000US-0177334P.
 XX 28-JAN-2000; 2000US-0178884P.
 XX 02-FEB-2000; 2000US-0179903P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Yang J, Baughn MR, Burford N, Au-Young J, Lu DM, Reddy R;
 PI Yue H, Nguyen DB, Tang YT, Yao MG, Lai P;
 XX WPI; 2001-418080/44.
 XX N-PSDB; AAD09549.
 XX
 XX Novel human protease proteins (PRTS) useful for diagnosing, treating,
 PT preventing gastrointestinal, cardiovascular, autoimmune/inflammatory,
 PT cell proliferative disorders associated with abnormal expression of PRTS.

PS Claim 1, Page 118, 129pp; English.

XX The present sequence is human protease protein (PRTS-12). Human PRTS and
 CC its nucleic acid molecule are useful for the diagnosis, treatment and
 CC prevention of disorders associated with increased or decreased expression
 CC of PRTS. Examples of such disorders include, gastrointestinal disorder
 CC such as anorexia, dysphagia; cardiovascular disorder such as
 CC atherosclerosis, vasculitis; autoimmune/inflammatory disorder such as
 CC acquired immune deficiency syndrome (AIDS), asthma; cell proliferative
 CC disorder such as actinic keratosis, cirrhosis; developmental disorder
 CC such as epilepsy, anaemia; epithelial disorder such as allergic contact
 CC dermatitis, eczema; neurological disorder such as Alzheimer's disease,
 CC dementia and reproductive disorder such as infertility and teratogenesis.
 CC PRTS DNA is useful for creating 'knockin' humanised animals (pigs) or
 CC transgenic animals (mice or rats) to model human disease. PRTS DNA is
 CC also in useful in gene therapy. PRTS and its immunogenic fragments are
 CC useful for screening libraries of compounds in several drug screening
 CC assays. PRTS is useful for analysing the proteome of a tissue or cell
 CC type

XX Sequence 414 AA;

Query Match 100.0%; Score 2130; DB 4; Length 414;
 Best Local Similarity 100.0%; Pred. No. 4.4e-181;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVLITLVKGLKPSFSPRYKALSEVQGMKORMAAKELARQNDLGFKLL 60
 DB 1 MNPTGLAIFLAVLITLVKGLKPSFSPRYKALSEVQGMKORMAAKELARQNDLGFKLL 60

QY 61 KKLAFNPGRNIFLPLSISTAFSMLCIGAQDSTLDEIKOGFNPFRKPEKDLHEGFHYII 120
 DB 61 KKLAFNPGRNIFLPLSISTAFSMLCIGAQDSTLDEIKOGFNPFRKPEKDLHEGFHYII 120

QY 121 HELTQKTQDLKLSIGNTLFIIDRLQPKRFLBDANKFYSAEITLITNFOULEMAQKQINDP 180
 DB 121 HELTQKTQDLKLSIGNTLFIIDRLQPKRFLBDANKFYSAEITLITNFOULEMAQKQINDP 180

QY 181 ISQKTHGKINNIENIDPGTVMLANVIFPRARWKHEPDNVTKEEFLFKNSSSVKVPV 240
 DB 181 ISQKTHGKINNIENIDPGTVMLANVIFPRARWKHEPDNVTKEEFLFKNSSSVKVPV 240

QY 241 MFRSGIYGVGYDDKLSCTTLEIPIYQKNITAIFILPDEGKHLKELKQVDTFSRWKTLIS 300

Db 241 MFRSGIYQVGYDDKLSCTIIIEIPYOKNITAFILPDEGKLHLEKGLQVDTFSWKTLIS 300
 QY 301 RRVVDVSVPRLHMTGTEDLKKTLSTYIGVSKI FEHGGDLTKIAPRSLKVGSAVHKAEIKM 360
 Db 301 RRVVDVSVPRLHMTGTEDLKKTLSTYIGVSKI FEHGGDLTKIAPRSLKVGSAVHKAEIKM 360
 QY 361 DERGTGAGAGTGAQTLPMEETPLVVKIDKPYLLLIYSEKIPSVLFLGKIIVPIGK 414
 Db 361 DERGTGAGAGTGAQTLPMEETPLVVKIDKPYLLLIYSEKIPSVLFLGKIIVPIGK 414
 RESULT 3
 ADA57300
 ID ADA57300 standard; protein; 414 AA.
 XX ADA57300;
 AC
 XX 20-NOV-2003 (first entry)
 DT
 XX
 DE Human secreted protein #583.
 KW immunosuppressive; antiinflammatory; antiaesthetic; antiallergic;
 KW cyclostatic; cerebroprotective; neuroprotective; nootropic;
 KW cardiovascular; antiarteriosclerotic; gene therapy;
 KW human secreted protein; immune disorder; inflammation;
 KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
 KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
 KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
 KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
 KW triple helix formation; antisense gene therapy; forensic biology.
 OS Homo sapiens.
 XX
 PN W02002102994-A2.
 XX
 PD 27-DEC-2002.
 XX
 PF 19-MAR-2002; 2002WC-US008278.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0311287P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2003-167512/16.
 DR N-PSDB; ADA56404.
 XX
 XX
 PT New human secreted polypeptides and polynucleotides, useful for
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
 PT conditions, respiratory disorders, cancers, CNS disorders, or
 PT neurodegenerative disorders.
 PS
 XX Claim 13; SEQ ID NO 1490; 1754bp; English.
 CC The invention relates to 592 new human secreted polypeptides useful for
 CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
 CC conditions, respiratory disorders, cancers, CNS disorders, or
 CC neurodegenerative disorders, or polypeptides comprising an amino acid
 CC sequence at least 95% identical to the new sequences. The polypeptides,
 CC antibodies or antibody fragments that bind to the polypeptides, nucleic
 CC acids encoding the polypeptides, agonists or antagonists that binds to
 CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
 CC compositions for diagnosing, treating or preventing an e.g. immune
 CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
 CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
 CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
 CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
 CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The

CC polynucleotides are useful for chromosome identification, chromosome
 CC mapping, for controlling gene expression through triple helix formation
 CC or antisense DNA or RNA, in gene therapy, for identifying individuals
 CC from minute biological samples, in forensic biology, and as hybridization
 CC probes. The polypeptides are useful for as molecular weight markers on
 CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
 CC gels, to raise antibodies, for testing biological activities, and for
 CC treating or preventing neural disorders, immune system disorders,
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal, proliferative and/or cancerous diseases. This sequence corresponds
 CC to one of the polypeptide of the invention. Note: The sequence data for
 CC this patent did form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 414 AA;
 Query Match 100.0%; Score 2130; DB 6; Length 414;
 Best Local Similarity 100.0%; Pred. No. 4,4e-181;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNPTLGAIPLAVLLITKGLIKSPSPRNKALSEVQGMQRMAAKELARQNDLGRKL 60
 Db 1 MNPTLGAIPLAVLLITKGLIKSPSPRNKALSEVQGMQRMAAKELARQNDLGRKL 60
 QY 61 KGLAFVNGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNPKMPEKDLHGFHYII 120
 Db 61 KGLAFVNGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKQGFNPKMPEKDLHGFHYII 120
 QY 121 HELTOKTQDLKLSIGNTLFLIDRLQPORKELEDAKNFSAETLLTNFONLEMAQKQINDF 180
 Db 121 HELTOKTQDLKLSIGNTLFLIDRLQPORKELEDAKNFSAETLLTNFONLEMAQKQINDF 180
 QY 181 ISQKTHGKINNLLENIDPGVNLANTIFFRANKHFPDNYTKSEDFLEKSSVYVPM 240
 Db 181 ISQKTHGKINNLLENIDPGVNLANTIFFRANKHFPDNYTKSEDFLEKSSVYVPM 240
 QY 241 MFRSGIYQVGYDDKLSCTIIIEIPYOKNITAFILPDEGKLHLEKGLQVDTFSWKTLIS 300
 Db 241 MFRSGIYQVGYDDKLSCTIIIEIPYOKNITAFILPDEGKLHLEKGLQVDTFSWKTLIS 300
 QY 301 RRVVDVSVPRLHMTGTEDLKKTLSTYIGVSKI FEHGGDLTKIAPRSLKVGSAVHKAEIKM 360
 Db 301 RRVVDVSVPRLHMTGTEDLKKTLSTYIGVSKI FEHGGDLTKIAPRSLKVGSAVHKAEIKM 360
 QY 361 DERGTGAGAGTGAQTLPMEETPLVVKIDKPYLLLIYSEKIPSVLFLGKIIVPIGK 414
 Db 361 DERGTGAGAGTGAQTLPMEETPLVVKIDKPYLLLIYSEKIPSVLFLGKIIVPIGK 414
 RESULT 4
 ADA41179
 ID ADA41179 standard; protein; 414 AA.
 XX
 AC ADA41179;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted protein.
 KW Human; secreted protein; cancer; hyperproliferative disorder;
 KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
 KW anaemia; allergic reaction; asthma; cardiovascular disorder;
 KW wound healing; cyclostatic; immunosuppressive; nootropic; neuroprotective;
 KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
 KW vulnerary; cardiac; gene therapy.
 OS Homo sapiens.
 XX
 PN W02002102993-A2.
 XX
 XX 27-DEC-2002.
 XX

QY	241	MRSRSGIYGVGDKXLSCTLIEIPYQKNITAFILFLPBGGLKHLKELGQVDPFSRMTLLS	3000
Db	241	MRSRSGIYGVGDKXLSCTLIEIPYQKNITAFILFLPBGGLKHLKELGQVDPFSRMTLLS	3000
QY	301	REVVDSVRLHMTGTFPDLKLTLSYIGVSKIFEEHDLTXIAPHRSILKGEAVHKAELKM	3600
Db	301	REVVDSVRLHMTGTFPDLKLTLSYIGVSKIFEEHDLTXIAPHRSILKGEAVHKAELKM	3600
QY	361	DERGTGGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIVNPICK	414
Db	361	DERGTGGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIVNPICK	414
RESULT 6			
ID	AAV86217	standart; protein; 415 AA.	
AC	AAV86217;		
XX	19-APR-2000	(first entry)	
DE	Human secreted protein HMHGUS4, SEQ ID NO:132.		
KW	Human; secreted protein; cancer; tumour; developmental abnormality;		
KW	foetal deficiency; blood disorder; immune system disorder; inflammation;		
KW	autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;		
KW	schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;		
KW	atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;		
KW	digestive disorder; endocrine disorder; infection; AIDS; leukaemia;		
XX	therapy.		
OS	Homo sapiens.		
XX	WO9966041-A1.		
XX	23-DEC-1999.		
XX	15-JUN-1999;	99WO-US013418.	
XX	16-JUN-1998;	98US-0089507P.	
PR	16-JUN-1998;	98US-0089508P.	
PR	16-JUN-1998;	98US-0089509P.	
PR	16-JUN-1998;	98US-0089510P.	
PR	22-JUN-1998;	98US-0090112P.	
PR	22-JUN-1998;	98US-0090113P.	
XX	(HUMA-) HUMAN GENOME SCI INC.		
PI	Soppen SM, Ni J, Rosen CA, Wei Y, Young PE, Florence KA,		
PI	Soppen DR, Brewer LA, Endress GA, Carter KC, Mucenaki M, Edner R;		
PI	Lafleur DW, Olsen HS, Shi Y, Moore PA, Komatsuils G;		
XX	WPI; 2000-106100/09.		
DR	N-PSDB; AAZ97021.		
PT	New isolated human genes and the secreted polypeptides they encode,		
PT	useful for diagnosis and treatment of e.g. cancers, neurological		
PT	disorders, immune diseases, inflammation or blood disorders.		
PS	Claim 1; Page 389-390; 586pp; English.		
XX	AAZ97019 to AAZ97137 represent 94 isolated human secreted protein genes.		
CC	AAH86215 to AAV86333 are the secreted proteins encoded by the 94 human		
CC	genes. This sequence represents a fragment of one of the human secreted		
CC	proteins. The genes and their corresponding secreted polypeptides are		
CC	useful for preventing, treating or ameliorating medical conditions, e.g.,		
CC	by protein or gene therapy. Also pathological conditions can be diagnosed		
CC	by determining the amount of the new polypeptides in a sample or by		
CC	determining the presence of mutations in the new genes. Specific uses are		
CC	described for each of the 94 genes, based on which tissues they are most		
CC	highly expressed in, and include developing products for the diagnosis or		
CC	treatment of cancer, tumours, developmental abnormalities and foetal		

CC	deficiencies, blood disorders, diseases of the immune system, autoimmune
CC	diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC	schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
CC	atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC	digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC	also useful for identifying their binding partners. The sequences shown
CC	in AAY69334 to AAY8585 represent fragments of the secreted proteins
XX	
SQ	Sequence 415 AA;
	Query Match 100.0%; Score 2130; DB 3; Length 415;
	Best Local Similarity 100.0%; Pred. No. 4,4e-181;
	Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MNPTGLAIFLAVALITVNGLLKPSPPNNYQLSEVGCKRMMAKEIARONMDLGFLL 60
DB	1 MNPTGLAIFLAVALITVNGLLKPSPPNNYQLSEVGCKRMMAKEIARONMDLGFLL 60
QY	61 KKLAFYNPGRIPLSPSLSTAFSMCLGAODSTLDEIKOGFNPKPEKOLHGFHYII 120
DB	61 KKLAFYNPGRIPLSPSLSTAFSMCLGAODSTLDEIKOGFNPKPEKOLHGFHYII 120
QY	121 HELTOKTDLKLSIGNTFLFDORLOPORKTEDAKNFYSAETIITNFOLEMAKOINDF 180
DB	121 HELTOKTDLKLSIGNTFLFDORLOPORKTEDAKNFYSAETIITNFOLEMAKOINDF 180
QY	181 ISOKTHGKINLIENIDPGTMLANTYFFPARKHEDPVYTEBEPFEKNSVVYPM 240
DB	181 ISOKTHGKINLIENIDPGTMLANTYFFPARKHEDPVYTEBEPFEKNSVVYPM 240
QY	241 MFRSGIVGVDDKLSTCILEIPYOKNITALFIILPDSEKLGHLKEKGLOVDTFSSWKTLIS 300
DB	241 MFRSGIVGVDDKLSTCILEIPYOKNITALFIILPDSEKLGHLKEKGLOVDTFSSWKTLIS 300
QY	301 RRVVDVSFRLAMGTGTPDLKKTLSYIGYSKIFEKHGDLTKAPRSLKVGEAVHKAELKM 360
DB	301 RRVVDVSFRLAMGTGTPDLKKTLSYIGYSKIFEKHGDLTKAPRSLKVGEAVHKAELKM 360
QY	361 DERGTGGAGGAGAOQLPMETPLVVKRIDEYPYLITYSEKIPSVLFLAGIVNPDGK 414
DB	361 DERGTGGAGGAGAOQLPMETPLVVKRIDEYPYLITYSEKIPSVLFLAGIVNPDGK 414
RESULT 7	
AEO53360	
ID	ABO53360 standard; protein; 415 AA.
XX	
AC	ABO53360;
XX	
DT	06-NOV-2003 (first entry)
XX	
DE	Novel human secreted protein #3.
XX	
KM	Human; vaccine; immune system disorder; haematopoietic cell disorder;
KM	cancer; autoimmune disorder; rheumatoid arthritis; glomerulonephritis;
KM	HIV infection; anaemia; thrombocytopenia blood coagulation disorder;
KM	blood platelet disorder; wound; heart attack; myocardial infarction;
KM	stroke; scarring; asthma; graft-versus host rejection; inflammation;
KM	hyperproliferative disorder; lymphoproliferative disorder; arrhythmia;
KM	aberrant cellular division; cell proliferative disorder; angiogenesis;
KM	cardiovascular disorder; pulmonary heart disease; neovascularisation;
KM	hypertrophic scar; keloid; ocular disorder; diabetic retinopathy;
KM	uveitis; epithelial cell proliferation; neurological disease; apoptosis;
KM	Parkinson's disease; Alzheimer's disease; Huntington's chorea; AIDS;
KM	amyotrophic lateral sclerosis; toxin induced liver disease; septic shock;
KM	cachexia; anorexia; lung damage; infection.
XX	
OS	Homo sapiens.
XX	
PN	US2003065151-A1.
XX	
PD	03-APR-2003.
XX	

PF 04-APR-2002; 2002US-00115123.
XX 16-JUN-1998; 98US-0089507P.
PR 16-JUN-1998; 98US-0089508P.
PR 16-JUN-1998; 98US-0089509P.
PR 16-JUN-1998; 98US-0089510P.
PR 22-JUN-1998; 98US-0090112P.
PR 22-JUN-1998; 98US-0090113P.
PR 15-JUN-1999; 99MO-US013418.
PR 14-DEC-1999; 99US-00461325.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Ni J, Rosen CA, Wei Y, Young P, Florence K, Soppet DR,
PI Brewer LA, Endress GA, Carter KC, MucenSKI M, Ebner R, Lafleur DW,
PI Olsen H, Shi Y, Moore PA, Komatsu G,
XX
DR MPI; 2003-531726/50.
XX N-PSDB; ACH66650.
XX
PT Novel antibody that binds specifically to a HCEJ069 protein, useful for
PT detecting the presence of a protein in a biological sample, and for
PT treating cancers, autoimmune disorders and HIV infection.
XX
PS Disclosure; SEQ ID NO 134; 176bp; English.
XX
XX The invention relates to an isolated antibody or its fragment that
CC specifically binds to a protein. The antibody is useful for detecting a
CC protein in a biological sample, by contacting the biological sample with
CC the antibody or its fragment and detecting the protein in the biological
CC sample. The antibody is useful for purifying, detecting and targeting the
CC human secreted proteins, including both in vitro and in vivo diagnostic
CC and therapeutic methods. The antibody is useful for immunophenotyping of
CC cell lines in biological samples and in antibody-based therapies for
CC treating, inhibiting and preventing diseases, disorders or conditions
CC associated with aberrant expression and/or activity of the above
CC proteins. The antibody is useful for treating deficiencies or disorders
CC of immune system and hematopoietic cells, for increasing differentiation
CC and proliferation of haematopoietic cells, for treating immune
CC deficiencies or disorders e.g. cancers, autoimmune disorders (such as
CC rheumatoid arthritis and glomerulonephritis), HIV infection, anaemia and
CC thrombocytopenia and as a marker for a particular immune system disease
CC or disorder. The antibody is also useful for treating blood coagulation
CC disorders, blood platelet disorders, wounds, heart attacks (infarction),
CC strokes, scarring and asthma. The antibody is also useful for treating or
CC preventing graft-versus host rejection, for modulating inflammation, for
CC treating hyperproliferative disorders e.g. lymphoproliferative disorders
CC and cancers, for inhibiting aberrant cellular division and for treating
CC cell proliferative disorders. The antibody is also useful for treating
CC cardiovascular disorders e.g. pulmonary heart disease and arrhythmia,
CC disorders associated with neovascularisation and angiogenesis, for
CC treating hypertrophic scars and keloids, ocular disorders e.g. diabetic
CC retinopathy and uveitis, for wound healing and disorders of epithelial
CC cell proliferation. The antibody is also useful for treating neurological
CC diseases e.g. Parkinson's disease, Alzheimer's disease, Huntington's
CC chorea and amyotrophic lateral sclerosis (ALS), diseases associated with
CC increased apoptosis e.g. AIDS, toxin induced liver disease, septic shock,
CC cachexia and anorexia, for preventing and healing damage to lungs and for
CC treating infectious diseases. The present sequence represents the amino
CC acid sequence of a novel human secreted protein. Note: the sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030065151
XX
SQ Sequence 415 AA;
Query Match 100.0%; Score 2130; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 4,4e-181;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 KGLAFYNGRNIFPLSPISISTAFSMLCLAQDSTLDBIKQGFNRKMPKEDLHEGFYII 120
DB 61 KGLAFYNGRNITLSPISISTAFSMLCLAQDSTLDBIKQGFNRKMPKEDLHEGFYII 120
QY 121 HELTQKTDKLSIGNTLFLDQRLQPKFLEDAKNFYSAETILTNFONLEMAQKQINDF 180
DB 121 HELTQKTDKLSIGNTLFLDQRLQPKFLEDAKNFYSAETILTNFONLEMAQKQINDF 180
QY 181 ISQKTHGKINNTLENDPGVMTLLANYIFPRARKHKEPDPNTKEDDFLEKSSVYVPM 240
DB 181 ISQKTHGKINNTLENDPGVMTLLANYIFPRARKHKEPDPNTKEDDFLEKSSVYVPM 240
QY 241 MFRSGIYGVYDDKLSCTTLEIPYQKNITAFILPDEGKLKHEKGLQVDTFSRMWTLIS 300
DB 241 MFRSGIYGVYDDKLSCTTLEIPYQKNITAFILPDEGKLKHEKGLQVDTFSRMWTLIS 300
QY 301 RRVADVSVPLNMTGTFDLKKTLSYIGVSKIFREHGDLTAKIAPHRSLSKGEAVHKAELKM 360
DB 301 RRVADVSVPLNMTGTFDLKKTLSYIGVSKIFREHGDLTAKIAPHRSLSKGEAVHKAELKM 360
QY 361 DERGTGAAGTGAQTLPMTPLVYKIDKPYLLIYSEKIPSVLFLGKIVNPIGK 414
DB 361 DERGTGAAGTGAQTLPMTPLVYKIDKPYLLIYSEKIPSVLFLGKIVNPIGK 414
RESULT 8
ID AAM78898 standard; protein; 414 AA.
XX AAM78898;
AC AAM78898;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1560.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
XX 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HUSB-) HUSB INC.
XX
XX Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QH, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW,
PI Xue AJ, Yang Y, Wejman T, Goodrich R,
XX
DR MPI; 2001-476283/51.
DR N-PSDB; AAK52031.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
PT
PS Claim 20; Page 3878-3879; 6221bp; English.
PS
XX The invention relates to polynucleotides (AAK51456-AAK5435) and the

CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK5581), 2111
 CC (AAK5582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 XX Sequence 414 AA;

Query Match 99.7%; Score 2123; DB 4; Length 414;
 Best Local Similarity 99.8%; Pred. No. 1.8e-180;
 Matches 413; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTLGLAIFLAVALLVKGLKSPSPRYKALSEVOGKQMAAKELARONMDLGFYII 60
 DB 1 MNPTLGLAIFLAVALLVKGLKSPSPRYKALSEVOGKQMAAKELARONMDLGFYII 60
 QY 61 KKLAFYNGRNIFLSPISITAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHEGFYII 120
 DB 61 KKLAFYNGRNIFLSPISITAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHEGFYII 120
 QY 121 HEITQKTDKLSIGNTLFTDORLQPKRKELEAKNAYSAETITNFQNTLMAQKQINDF 180
 DB 121 HEITQKTDKLSIGNTLFTDORLQPKRKELEAKNAYSAETITNFQNTLMAQKQINDF 180
 QY 181 ISQTKGKINMLIENIDPGTVMLLANYIPFRARKHEFDNVYKEEPFLKSSVAVPM 240
 DB 181 ISQTKGKINMLIENIDPGTVMLLANYIPFRARKHEFDNVYKEEPFLKSSVAVPM 240
 QY 241 MFRSGIYQVGYDDKLSCTILIEFYQXNITAFILPDEGKLKHEKGLQVDFSMKTLIS 300
 DB 241 MFRSGIYQVGYDDKLSCTILIEFYQXNITAFILPDEGKLKHEKGLQVDFSMKTLIS 300
 QY 301 RRVVADVSPRLHMTGTPFDLKKTSYIGVSKLFFRHHGLTLIAHRSKAGBAVHAKELM 360
 DB 301 RRVVADVSPRLHMTGTPFDLKKTSYIGVSKLFFRHHGLTLIAHRSKAGBAVHAKELM 360
 QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKISPVFLGIKIVPIGK 414
 DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKISPVFLGIKIVPIGK 414

RESULT 9
 ABB11832
 ID ABB11832 standard; peptide; 431 AA.

XX
 AC ABB11832;
 XX
 DT 11-JAN-2002 (first entry)
 XX

DE Human secreted protein homologue, SEQ ID NO:2202.

KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulatory; activin;
 KW inhibin; chemokinesis; chemokinesis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antistatic; antiarthritis; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteoprotic; vasotrophic; cardiac; vitruce; antibacterial;
 KW antifungal; vulnerary; antitumor.

OS Homo sapiens.

XX
 XX W0200157188-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 05-FEB-2001; 2001WO-US003800.
 XX
 XX 03-FEB-2000; 2000US-00496914.
 XX 27-APR-2000; 2000US-00560875.
 XX
 XX (HYSR-) HYSRQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT;
 XX
 XX WPI: 2001-457740/49.
 XX
 XX N-PSDB; ABA09076.
 XX
 XX Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 XX Claim 20; Page 263; 1963pp; English.

XX
 XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 XX

SO Sequence 431 AA;

Query Match 99.7%; Score 2114; DB 4; Length 431;
 Best Local Similarity 99.3%; Pred. No. 1.2e-179;
 Matches 411; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNPTLGLAIFLAVALLVKGLKSPSPRYKALSEVOGKQMAAKELARONMDLGFYII 60
 DB 18 MNPTLGLAIFLAVALLVKGLKSPSPRYKALSEVOGKQMAAKELARONMDLGFYII 77
 QY 61 KKLAFYNGRNIFLSPISITAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHEGFYII 120

Db 78 KKLAFYNPGRNIFLSPISISTAFSMCLGAQDSTLDEIKQGFNFRKMPKDLHEGFHYII 137
 QY 121 HELTQKTQDLKLSIGNTLFIIDQRLQPKRFLBDAKNFYSAETILTNFQNLMAQKQINDF 180
 Db 138 HELTQKTQDLKLSIGNTLFIIDQRLQPKRFLBDAKNFYSAETILTNFQNLMAQKQINDF 197
 QY 181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRARWKHEPDNPVTKEDDFLEKNSVYKVPW 240
 Db 198 IESKTHGKINNLIENIDPGTVMLLANYIFPRARWKHEPDNPVTKEDDFLEKNSVYKVPW 257
 QY 241 MFRSGIYQVGYDQKLSCTTLEIPIYQKNITAFILPDEGKLHLEKGLQVDFSRMKTLLS 300
 Db 258 MFRSGIYQVGYDQKLSCTTLEIPIYQKNITAFILPDEGKLHLEKGLQVDFSRMKTLLS 317
 QY 301 RRVVDVSVPLHMTGTFDLKKTLSYIGSVKIFEEHGDLTAKIAPHRSLSKVGEAVHKAELKM 360
 Db 318 RRVVDVSVPLHMTGTFDLKKTLSYIGSVKIFEEHGDLTAKIAPHRSLSKVGEAVHKAELKM 377
 QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
 Db 378 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 431

RESULT 10

AAW79882
ID AAW79882 standard; protein; 431 AA.

AC AAW79882;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 3528.

KM Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KM tissue growth factor; immunomodulatory; cancer; leukaemia;

KM nervous system disorder; arthritis; inflammation.

OS Homo sapiens.

PN WO200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US004098.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00596075.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-0064936.

PR 15-SEP-2000; 2000US-00664961.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

PA (HYSE-) HYSEQ INC.

PI Tang YF, Liu C, Drmanac RR, Asundi V, Zhou P, Xu C, Cao Y;

PI Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

DR WPI, 2001-476283/51.

DR N-PSDB; AAKS3015.

PS Nucleic acids encoding polypeptides with cytokine-like activities, useful

PS in diagnosis and gene therapy.

PS Claim 20; Page 371; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the

XX encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to

XX cytokine, cell proliferation or cell differentiation or which may induce

XX production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52561), 2111
 CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX

SO Sequence 431 AA;

Query Match 99.2%; Score 2114; DB 4; Length 431;

Best Local Similarity 99.3%; Pred. No. 1.2e-179;

Matches 411; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNPITGLAIFLAVLTVKGLKPSRPNRYKALSTVQWKQMAAKELARQNDLGFKL 60
 Db 18 MNPITGLAIFLAVLTVKGLKPSRPNRYKALSTVQWKQMAAKELARQNDLGFKL 77
 QY 61 KKLAFYNPGRNIFLSPISISTAFSMCLGAQDSTLDEIKQGFNFRKMPKDLHEGFHYII 120
 Db 78 KKLAFYNPGRNIFLSPISISTAFSMCLGAQDSTLDEIKQGFNFRKMPKDLHEGFHYII 137
 QY 121 HELTQKTQDLKLSIGNTLFIIDQRLQPKRFLBDAKNFYSAETILTNFQNLMAQKQINDF 180
 Db 138 HELTQKTQDLKLSIGNTLFIIDQRLQPKRFLBDAKNFYSAETILTNFQNLMAQKQINDF 197
 QY 181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRARWKHEPDNPVTKEDDFLEKNSVYKVPW 240
 Db 198 IESKTHGKINNLIENIDPGTVMLLANYIFPRARWKHEPDNPVTKEDDFLEKNSVYKVPW 257
 QY 241 MFRSGIYQVGYDQKLSCTTLEIPIYQKNITAFILPDEGKLHLEKGLQVDFSRMKTLLS 300
 Db 258 MFRSGIYQVGYDQKLSCTTLEIPIYQKNITAFILPDEGKLHLEKGLQVDFSRMKTLLS 317
 QY 301 RRVVDVSVPLHMTGTFDLKKTLSYIGSVKIFEEHGDLTAKIAPHRSLSKVGEAVHKAELKM 360
 Db 318 RRVVDVSVPLHMTGTFDLKKTLSYIGSVKIFEEHGDLTAKIAPHRSLSKVGEAVHKAELKM 377
 QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414
 Db 378 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 431

RESULT 11

AAU05759
ID AAU05759 standard; protein; 358 AA.

AC AAU05759;

DT 24-OCT-2001 (first entry)

DE Human NOV7 polypeptide #2.

KM Human; NOV7; A132990 B; fertility disorder; spermatogenesis; cardiant;

KM cytostatic; immunomodulatory; antiproliferative; antidiabetic;

KM cell proliferation; cancer; diabetic retinopathy; angiodysplasia;

KM pulmonary disorder; haematopoietic disorder; immunological disorder;

KM inflammatory disorder; tumour related disorders; emphysema; cirrhosis;

KM wound healing; gene therapy.

OS Homo sapiens.

FT Key location/Qualifiers

FT Misc-difference 311..322

FT /label= OTHER

PN WO200149729-A2.

PD 12-JUL-2001.

[illegible]

```

AAP50877
ID AAP50877 standard; protein; 418 AA.
XX
XX AAP50877?
XX
DT 25-MAR-2003 (revised)
DT 16-AUG-2002 (revised)
DT 03-SEP-1991 (first entry)
XX
DE Sequence encoded by human alpha-1-antitrypsin (alpha-1-AT) cDNA.
XX
KM Leukocyte elastase inhibitor; emphysema therapy; lung disease.
XX
OS Homo sapiens.
OS Synthetic.
XX
Key Location/Qualifiers
FT Misc-difference 125 /note= "Arg in published SQ"
FT FT 139 /note= "Asp in published SQ"
FT Misc-difference 140 /note= "Gly in published SQ"
FT FT 237 /note= "Ala in published SQ"
FT FT 273 /note= "Asn in published SQ"
FT Misc-difference 326 /note= "Val in published SQ"
FT FT 382, 383 /label= Reactive centre
XX
Region
FT EP164719-A.
FN EN
XX PD
XX 18-DEC-1985.
PF 14-JUN-1984; 84US--00620408.
PR 14-JUN-1984; 84US--00620408.
PR 14-JUN-1984; 84US--00620662.
PA (CHIR ) CHIRON CORP.
PI Barr PJ, Hallewell RA, Rosenberg S, Brake AJ,
FI WPI, 1985-318257/51.
DR N-PSDB; AAN50540.
XX
PT Polypeptide oxidative stable serine protease inhibitor - having human
PT alpha-1-antitrypsin amino-acid sequence with neutral amino-acid at active
site.
XX
PS Example; Page 16; 37pp; English.
XX
CC The inventors claim a polypeptide oxidative stable human leukocyte
CC elastase inhibitor differing from wild type human alpha-1-AT by fewer
CC than 10 AAs and having the methionine at the active site (see AAP50877)
CC substituted with a neutral oxidatively stable AA, pref. Val or Ala.
CC CC (Updated on 16-AUG-2002 to add missing OS field.) (Updated on 25-MAR-2003
to correct PA field.)
XX
XX SQ
Sequence 418 AA;

Query Match 37.3%; Score 795; DB 1; Length 418;
Best Local Similarity 43.0%; Pred. No. 6.3e-62;
Matches 156; Conservative 74; Mismatches 131; Indels 2; Gaps 1

54 DLGFLKKQLAFYNGRNIFLSPISISTAFSMTLCGAQDSTLDKIKGFNFR--IMPEKD 111
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
56 EFAPSLVRLAHHSNSTVFSPYSIAFAFMTLSGTADTHDELLEGINFVLTEIPEAQ 115
||||| ||||| : : : : : : : : : : : : : : : : : : : : : :
112 LHGEFYIIHLLTOKTDKLSTGNLTFLFDRLQDPORFFLEDANKFYSAETILTNPNQLE 171
: ||||| : : : : : : : : : : : : : : : : : : : : : :

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DB 116 IHGFOQLHTLNQPSQQLTGTNGFLPSBGLKLVDFLEBDVKCLYHSEAFVTFNGDTE 175
QY 172 MAQKQINDPISQKTHKINNLINIPGTYMLANITFFPAARKHEFDNVTKEEDFPLE 231
DB 176 EAKKQINDVVEKGTQKIDVLYKELDRHTVFAVNIFFPKGWERPEVVDTEEDFHYD 235
QY 232 KNSSVKVPMMFRRSGIYQVGYDDKLSCTILEIPYOKNITAFILPDEGKLKHEKGLOVD 291
DB 236 QVTTVAVPMMKRLGMNIGHCKKLSWVLMKYLGNATAFILPDEGKLOHLENELTHDI 295
QY 292 FSRWKTLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKLFEHGDULTIAHRSKJVE 351
DB 296 ITRFLENEDRRSASLHLPKLSTIGTYDLKSLGQLGITTKVFSNGADLSGVTGQAPKLK 355
QY 352 AVHKAEIKMDEGTGEGAAGTGAQTLPMETPLVYKIDKPYLLLYSEKIPSVFLGIQVNP 411
DB 356 AVHKAVLTIDEGKTEAAGMFLBAIPMSIPPEVKRNPFLMIEQNTSPFLMGKVNP 415
QY 412 ICK 414
DB 416 TCK 418

RESULT 13
AAV44205
ID AAV44205 standard; protein; 394 AA.
AC AAV44205;
XX 25-JAN-2000 (first entry)
DE Alpha-1 antitrypsin variant Pittsburgh.
XX Alpha-1 antitrypsin variant Pittsburgh; alpha-1 antitrypsin; PIT;
XX negative control; furin inhibition assay; peptide mimetic; A7 cell;
XX Pseudomonas aeruginosa exotoxin A; PEA; HCMV glycoprotein gB.
XX Synthetic.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 358 /note= "Wild type Met substituted by Arg"
XX MO9951624-A1.
XX 14-OCT-1999.
XX 08-APR-1999; 99WO-US007776.
XX 08-APR-1998; 98US-0081034P.
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX Jean F, Thomas G;
XX MPI; 1999-620190/53.
XX New furin endoprotease inhibitor that mimics a specific region of alpha-1
XX antitrypsin Portland mutant, for treatment and prevention of bacterial
XX and viral infection.
XX Example 1; Page 101-102; 108bp; English.
XX The present sequence is alpha-1 antitrypsin mutated variant Pittsburgh
XX (also termed PIT). PIT protein was used as a negative control in furin
XX inhibition assay to assess the biological activity of the peptide
XX mimetics. A7 cells when incubated with PIT exhibited little or no
XX protective effect in the presence of Pseudomonas aeruginosa exotoxin A.
XX PIT was also used as a negative control for the assay to detect PDX -
XX mediated inhibition of furin-catalysed maturation of HCMV glycoprotein gB
XX Sequence 394 AA;
```

```
Query Match 37.2%; Score 792; DB 2; Length 394;
Best Local Similarity 43.0%; Pred. No. 1,1e-61;
Matches 156; Conservative 72; Mismatches 133; Indels 2; Gaps 1;

QY 54 DLGFKLLKKAFLAPNPGRNIFLPSLSISTAFSMICGAQDSTIDEIKOGFNFR--KXPEKD 111
DB 32 EFAPSLYRQLAHQSNSTNIFSPVSIATFAFALISGTAKDTHDEILEGNFNLQLEPAQ 91
QY 112 LHGFFYITHEITQTKQDKLSIGNTLFLFDQLQPRKLEDAKNFYSAETILTNQONE 171
DB 92 IHGFOELRLTNQPSQQLTGTNGFLPSQGLKLVDFLEBDVKCLYHSEAFVTFNGDTE 151
QY 172 MAQKQINDPISQKTHKINNLINIPGTYMLANITFFPAARKHEFDNVTKEEDFPLE 231
DB 152 QAKKQINDVVEKGTQKIDVLYKELDRHTVFAVNIFFPKGWERPEVVDTEEDFHYD 211
QY 232 KNSSVKVPMMFRRSGIYQVGYDDKLSCTILEIPYOKNITAFILPDEGKLKHEKGLOVD 291
DB 212 QVTTVAVPMMKRLGMNIGHCKKLSWVLMKYLGNATAFILPDEGKLOHLENELTHDI 271
QY 292 FSRWKTLSRRVVDVSVPRLHMTGTFDLKKTLSYIGVSKLFEHGDULTIAHRSKJVE 351
DB 272 ITRFLENEDRRSASLHLPKLSTIGTYDLKSVLGQGITTKVFSNGADLSGVTGQAPKLK 331
QY 352 AVHKAEIKMDEGTGEGAAGTGAQTLPMETPLVYKIDKPYLLLYSEKIPSVFLGIQVNP 411
DB 332 AVHKAVLTIDEGKTEAAGMFLBAIPRSIPPEVKRNPFLMIEQNTSPFLMGKVNP 391
QY 412 ICK 414
DB 392 TCK 394
```

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RESULT 14
AAV44201
ID AAV44201 standard; protein; 394 AA.
AC AAV44201;
XX 25-JAN-2000 (first entry)
DE Alpha-1 antitrypsin variant Portland.
XX Alpha-1 antitrypsin variant Portland; alpha-1 antitrypsin; PD;
XX protease inhibitor; furin endoprotease; peptide mimetic; bacterial toxin;
XX furin recognition site; portland protein; SIBYL program; Pharmacophore;
XX protein crystal structure analysis; reactive site loop; RSL;
XX endolytic maturation; endoproteolytic activation; Pseudomonas aeruginosa;
XX Corynebacterium diphtheriae; Bacillus anthracis; cytomegalovirus;
XX biologically active protein.
XX Synthetic.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc-difference 355 /note= "Wild type Ala substituted by Arg"
FT Misc-difference 358 /note= "Wild type Met substituted by Arg"
XX MO9951624-A1.
XX 14-OCT-1999.
XX 08-APR-1999; 99WO-US007776.
XX 08-APR-1998; 98US-0081034P.
XX (UYOR-) UNIV OREGON HEALTH SCI.
XX Jean F, Thomas G;
XX
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Thu Apr 6 09:52:31 2006

us-10-664-356-1562.rag

Page 12

Qy 352 AVHKRELKMDRGSTGCAAGTGAQTLPMBETPLVYKTKIDKPYLLIYSSEKISVLEFGKIVNP 411
 Db 356 AVHKAVLTIDRGSTLGAAGMPLFALITFMSLPPEVYKFKPKPEVFLMIIEQNTISPLFMGKIVNP 415
 Qy 412 IGR 414
 Db 416 TOK 418

Search completed: March 31, 2006, 09:46:07
Job time : 192 secs

GenCore version 5.1.7
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OM protein - protein search, using bw model

Run on: March 31, 2006, 09:46:24 ; Search time 41 Seconds
(without alignments)
971.555 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 2130
Sequence: 1 MNPTGLAIFLAVLLTVKGL.....YSEKIPSVLFKGIKVPFGK 414

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	787	36.9	409	1 ITBA	alpha-1-antitrypsin
2	785.5	36.9	413	2 SS4981	alpha-1-antitrypsin
3	785	36.9	411	1 ITKT	alpha-1-antitrypsin
4	785	36.9	418	1 ITTU	alpha-1-antitrypsin
5	782	36.7	406	2 JX0346	alpha-1-antitrypsin
6	780.5	36.6	413	2 JX0154	alpha-1-antitrypsin
7	778.5	36.5	413	2 JX0267	alpha-1-antitrypsin
8	775.5	36.4	413	2 AS4968	alpha-1-antitrypsin
9	768.5	36.0	413	2 I49470	alpha-1-antitrypsin
10	766.5	35.7	413	2 I49472	alpha-1-antitrypsin
11	760.5	35.6	413	2 I49452	alpha-1-antitrypsin
12	758.5	35.6	413	2 I49471	alpha-1-antitrypsin
13	756	35.5	413	2 S60036	alpha-1-antitrypsin
14	753	35.4	413	2 S11320	alpha-1-antitrypsin
15	747.5	35.1	408	2 S11320	alpha-1-antitrypsin
16	745.5	35.0	416	2 B29131	alpha-1-antitrypsin
17	743	34.9	403	2 S08102	alpha-1-antitrypsin
18	742.5	34.9	413	2 I49474	alpha-1-antitrypsin
19	742	34.8	416	2 S21097	alpha-1-antitrypsin
20	731	34.3	418	1 S31507	alpha-1-antitrypsin
21	728.5	34.2	416	1 A39339	alpha-1-antitrypsin
22	728	34.2	406	1 ITSH	alpha-1-antitrypsin
23	726.5	34.1	418	2 JH0494	alpha-1-antitrypsin
24	725.5	34.1	410	2 A45457	alpha-1-antitrypsin
25	717	33.7	405	2 A39088	alpha-1-antitrypsin
26	716	33.6	383	2 A36117	alpha-1-antitrypsin
27	714	33.5	413	2 I56481	alpha-1-antitrypsin
28	710.5	33.4	418	2 S23615	alpha-1-antitrypsin
29	707	33.2	412	1 ITMSC	alpha-1-antitrypsin

30	702	33.0	418	2 JX0129	contrapsin precurs
31	701	32.9	412	2 S31505	serine proteinase
32	701	32.9	417	2 S19724	kallikrein-binding
33	698.5	32.8	415	2 A47224	thyroxine-binding
34	696	32.7	430	2 A49190	corticosteroid-bin
35	686	32.2	412	2 I46421	thyroxine-binding
36	685.5	32.2	418	2 A39567	thyroxine-binding
37	684.5	32.1	406	2 I53281	corticosteroid-bin
38	680	31.9	410	2 C39088	contrapsin precurs
39	678.5	31.9	433	1 ITTUC	alpha-1-antitrypsin
40	674	31.6	405	2 A28321	corticosteroid-bin
41	663	31.1	410	2 I50494	serine proteinase
42	651.5	30.6	388	2 B39088	alpha-1-antitrypsin
43	644.5	30.3	436	2 A42440	estrogen-regulated
44	629	29.5	427	2 A49518	kallikrein precurs
45	620.5	29.1	369	2 JH0493	alpha-1-antitrypsin

ALIGNMENTS

RESULT 1

ITBA
alpha-1-antitrypsin precursor - baboon (fragment)
N/Alternate names: alpha-1-proteinase inhibitor
C/Species: Papio sp. (baboon)
C/Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 05-Oct-2004
C/Accession: A01248
R/Kurachi, K.; Chandra, T.; Degen, S.J.F.; White, T.T.; Marchioro, T.L.; Woo, S.L.C.; Day
Proc. Natl. Acad. Sci. U.S.A. 78, 6826-6830, 1981
A/Title: Cloning and sequence of cDNA coding for alpha-1-antitrypsin.
A/Reference number: A01248; MUID:82082539; PMID:7031661
A/Accession: A01248
A/Molecule type: mRNA
A/Residues: 1-409 <KUR>
C/Cross-references: UNIPARC:UPI0000124FDC; GB:U00321; NID:G176561; PIDN:AAA5377.1; PID:
C/Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its primary target
psin.
C/Superfamily: serpin
C/Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
F/1-15/Domain: signal sequence (fragment) #status predicted <SIG>
F/16-409/Product: alpha-1-antitrypsin #status predicted <MAT>
F/61,98,262/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/373/Inhibitory site: Met (elastase, collagenase) #status predicted

Query Match	36.9%;	Score 787;	DB 1;	Length 409;
Best Local Similarity	41.9%;	Pred. No. 8e-47;		
Matches 152;	Conservative 82;	Mismatches 127;	Indels 2;	Gaps 1
QY	54	DLAGFKLLKLAFFNPGNIFLSPISISTAFSMLCAGADSITDEIKGFNFR--KMPKXD	111	
DB	47	EPAPSLYRQLAHOSNSTIFFSPVSITATPAMSLGKADTSHIELGNFNLTEIEAQ	106	
QY	112	LHSGFYIHELTOQTDLKLSIGNTLFIQDLOPOKFFEDAKNFSAETILTNFONLE	171	
DB	107	VHSGFQELATLTKPKPSQLQITNGELFLAKSLKVVVDKLEDDYKYLHSAFNSFVEEDTE	166	
QY	172	MAQKQINDFISQTHGKINNLINIDGTWLLANVIFPFAKWKHEFDNPVTKEDDFLE	231	
DB	167	EAKKQINNVYKGTQGVVDLVKELDRDVFALVANYIFFGKWKRPPEVATEEDPHVD	226	
QY	232	KNSSVYPMFBSGIVQVDDKLSCTIILEIPQKNTAIFILPDGKLLHLEKGLQVDT	291	
DB	227	QATTVKPMRRIRLGMNIVHCEKLSWVLLMKYLGNAITALFFLPDEKQLHLENELTHDI	286	
QY	292	FSRKKTLISRVDVSVPLAMTGFPLDKTSLYIGVSKIFSEHGDLTKIAPRSLKVG	351	
DB	287	ITTFLENENRNSANLHPKLAITGTVDLKVGLHGLITKFKSGADISGTEBAPLKSK	346	
QY	352	AVHKAELKQDERGTGGAAGTAQTLPMETPLVVKIDKPYLLLYSEKIPSVLFKGIKVP	411	
DB	347	AVHKAVALTDKGTGAAGMFLBALPMSIPEVKFNKPFVFLMIQWTKSPPLFGKVVNP	406	

Qy 412 IGR 414
Db 407 TQK 409

RESULT 2

S54981

alpha-1-antiprotease isoform B precursor - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 05-Oct-2004
C/Accession: S54981, S72199

R/Saito, A.; Sinohara, H.

Biochem. J. 307, 369-375, 1995

A/Title: Rabbit alpha-1-antiprotease B: a novel recombinant serpin which does not inhibit
A/Reference number: S54981, MID:95251597, PMID:7733871

A/Accession: S54981

A/Molecule type: mRNA

A/Residues: 1-413 <SA12>

A/Cross-references: UNIPROT:Q28665; UNIPARC:UPI0000086790; EMBL:D17725; MID:91008927; PI

A/Accession: S72199

A/Molecule type: protein

A/Residues: 25-33;374-387 <SA12>

A/Cross-references: UNIPARC:UPI0000176311; UNIPARC:UPI0000176312

C/Superfamily: serpin

C/Keywords: acute phase; emphysema; glycoprotein; plasma; serine protease inhibitor

F/1-24/Domain: signal sequence #status predicted <SIG>

F/25-413/Product: alpha-1-antiprotease B #status experimental <MAT>

Query Match

Best Local Similarity 36.9%; Score 785.5; DB 2; Length 413;
Matches 155; Conservative 98; Mismatches 155; Indels 5; Gaps 2;

Qy 1 MNPTGLAIFLAVLTWKGLKPSFSPRNKALSEVQGMKQMAAKELARQNMIDGFKLL 60
1 MPPSVRAL---LLAGLGLCLPGLFADAEQETAVSSHEDHACRIAPSLAPALSLX 57
Db 1 KGLAFNPGRNIFLPSLISSTAFSMCLGAQDSTLDEIKQG--FNPRKPEKDLHGCFHY 118
58 REVAHSNTNTNIFPFSVSIATAPAMLSIAKGDTHQVLEKFNLTETAEQIHQGFH 117
Qy 119 IHELTQKTQDCLKISGNTLFTDRLQPKRFEADAKNFYSATITLTNQNLEMAQKQIN 178
118 LHTATVRPDSQLQALAGNALVHVENIKLQHKFLEDAKNLYQSEAFVDFPDPAQATKIN 177
Db 179 DRTSQKTHKINNLINIDPGVMTLANYIFPRAKMHEFDPNVTKEEPEFLKSSVYK 238
178 SHVEKTRGKIYDVLVDELAKTILALVNVYFFGKKKEKPEPNTKEEDFHVDAITTVK 237
Qy 239 PMWFSGIYQVGYDDKLSCTTIEIPYQKNTAIFILPDEGKLHLEKGLQVDTFSRMTL 298
238 PMWSRLGMYVMEFCSSTLASTVLMYKGNATLFLPDEGKLQHLBDTLTTEIAKFLAK 297
Db 299 LSRVVDVSVRLHMTGTDFDKTSLYIGVSKIPEEHGDLTKAPRSLKVGAAVKAEL 358
298 SLIRSTYVFPKLSISGTYDLKPLGLKGLGTQVFSNNADLSGTGEDEPLKVSQALHKA 357
Qy 359 KMDERGTGGAAGAGTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIVNP 411
358 TIDERTGAAGASFVLEIPESVDSITIDRPFLEVIYSHKISPLFVGKVIDP 410
Db

RESULT 3

ITRT

alpha-1-antitrypsin precursor - rat

N/Alternate names: alpha-1-protease inhibitor

C/Species: Rattus norvegicus (Norway rat)

C/Date: 31-Mar-1992 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
C/Accession: A33892; B33892; S08016; JX0123; A38823

R/Chao, S.; Chai, K.X.; Chao, L.; Chao, J.

Biochemistry 29, 323-329, 1990

A/Title: Molecular cloning and primary structure of rat alpha-1-antitrypsin.

A/Reference number: A33892; MID:90148955; PMID:2302382

A/Accession: A33892

A/Molecule type: mRNA

A/Residues: 4-411 <CHA>

A/Cross-references: UNIPROT:P17475; UNIPARC:UPI0000170896; GB:M32247; MID:g203062; PIDN:J

A/Accession: B33892

A/Molecule type: protein

A/Residues: 25-57 <CH2>

A/Cross-references: UNIPARC:UPI00001731P9

R/Fink, I.L.; Bailey, T.; Morfin, B.

submitted to the EMBL Data Library, August 1989

A/Reference number: S08016

A/Accession: S08016

A/Molecule type: mRNA

A/Residues: 188-246; 'I', 248-321, 'D', 323-389 <FL1>

A/Cross-references: UNIPARC:UPI0000170827; EMBL:X16273; MID:957229; PIDN:CAA34349.1; PID:

R/Masuni, Y.; Sobda, M.; Ohkubo, K.; Takami, N.; Oda, K.; Ikehara, Y.

J. Biochem. 108, 230-234, 1990

A/Title: Molecular cloning and sequencing of the cDNA of rat alpha-1-protease inhibitor

A/Reference number: JX0123; MID:91035351; PMID:2229024

A/Accession: JX0123

A/Molecule type: RNA

A/Residues: 1-13; 'G', 15-83, 'V', 85-247, 'Y', 249-317, 'N', 319-411 <MIS>

A/Cross-references: UNIPARC:UPI000016797B; GB:D00675; MID:g220648; PIDN:BA00579.1; PID:

A/Experimental source: serum

A/Accession: A38823

A/Molecule type: protein

A/Residues: 25-45 <MI2>

A/Cross-references: UNIPARC:UPI00001731PA

C/Comment: Alpha-1-antitrypsin is an inhibitor of serine proteases. Its primary target

psin.

C/Superfamily: serpin

C/Keywords: acute phase; glycoprotein; plasma; serine protease inhibitor

F/1-24/Domain: signal sequence #status predicted <SIG>

F/25-411/Product: alpha-1-antitrypsin #status experimental

F/4,101,265/Binding site: carbohydrate (Asn) (covariant) #status predicted

F/376/Inhibitory site: Met (elastase, collagenase) #status predicted

Query Match 36.9%; Score 785; DB 1; Length 411;
Best Local Similarity 38.8%; Pred. No. 1,1e-46;
Matches 161; Conservative 94; Mismatches 150; Indels 10; Gaps 5;

Qy 1 MNPTGLAIFLAVLTWKGLKPSFSPRNKALSEVQGMKQMAAKELARQNMIDGFKLL 60
1 MAPSISRGILLALALC---CLAPSFLEADAQETPTSQDQSPYRKISSNLADFAFSLX 56
Db 61 KGLAFNPGRNIFLPSLISSTAFSMCLGAQDSTLDEIKQG--FNPRKPEKDLHGCFHY 118
57 RELVHOSNTSNIFPSPMSITTPAMLSLSSKQDTRKQILEGFNLTQLEPADIHKAFH 116
Qy 119 IHELTQKTQDCLKISGNTLFTDRLQPKRFEADAKNFYSATITLTNQNLEMAQKQIN 178
117 LQTLNRPDSQLQNTGNGLFVNKQIKLVEKFLIEVKNNYHSEAFSVNADSEBAKVIN 176
Db 179 DRTSQKTHKINNLINIDPGVMTLANYIFPRAKMHEFDPNVTKEEPEFLKSSVYK 238
177 DVEKGTQKQIDVLMKQLEDVTFALVNTIFPKGKKRPFNEHRDADFHVDKSTTVY 236
Qy 239 PMWFSGIYQVGYDDKLSCTTIEIPYQKNTAIFILPDEGKLHLEKGLQVDTFSRMTL 298
237 PMANRLGMDMYCTSLSSWVLMYLGNAATLFIPLPDGKKQHLQGITLQDLISRF--L 294
Db 299 LSR--RVVDVSVRLHMTGTDFDKTSLYIGVSKIPEEHGDLTKAPRSLKVGAAVKA 356
295 LNRQTSALIVPPKLSISGTYNLKTLISGLITRVFNNDADLSGTEDAPLKSQAVHKA 354
Qy 357 ELKMDERGTGGAAGAGTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIVNP 411
355 VLTLDERTGAAGATVVEAVPMSLPQVFDHPFIFMIVESQSPLEFVGKVIDP 409
Db

RESULT 4

ITRU

alpha-1-antitrypsin precursor [validated] - human

N/Alternate names: alpha-1-AI; alpha-1-protease inhibitor

C:Species: Homo sapiens (man)
C:Date: 30-Nov-1980 #sequence revision 31-Mar-1992 #text change 05-Oct-2004
A:Accession: A21853; B21853; A93352; A90944; A58528; A23174; A93281; A23336; S14476; A24
R:Long, G.L.; Chandra, T.; Woo, S.L.C.; Davie, E.W.; Kurachi, K.
A:Title: Complete sequence of the cDNA for human alpha-1-antitrypsin and the gene for th
A:Reference number: A21853; MUID:85047190; PMID:6093867
A:Accession: A21853
A:Molecule type: mRNA
A:Residues: 1-418 <LON1>
A:Cross-references: UNIPROT:P01009; UNIPARC:UP1000000CBEC; GB:K02212; NID:G177830
A:Experimental source: M (normal) allele
A:Accession: B21853
A:Molecule type: DNA
A:Residues: 1-287, 'V', 289-418 <LON2>
A:Cross-references: UNIPARC:UP1000016A3A8; GB:K02212; NID:G177830; PIDN:AA59495.1; PID:
A:Experimental source: S variant allele
R:Roederberg, S.; Barr, P.J.; Najarian, R.C.; Halliwell, R.A.
A:Title: Synthesis in yeast of a functional oxidation-resistant mutant of human alpha-1-
A:Reference number: A93352; MUID:85036645; PMID:6387509
A:Accession: A93352
A:Molecule type: mRNA
A:Residues: 1-124, 'H', 126-325, 'I', 327-418 <ROS>
A:Cross-references: UNIPARC:UP1000014DB5; EMBL:X01683; NID:G28965
R:Bollen, A.; Herzog, A.; Cravador, A.; Herion, P.; Chuchana, P.; Vander Straten, A.; Lo
DNA 2, 255-264, 1983
A:Title: Cloning and expression in Escherichia coli of full-length complementary DNA cod
A:Reference number: A90944; MUID:84107980; PMID:6319097
A:Accession: A90944
A:Molecule type: mRNA
A:Residues: 1-138, 'DG', 141-272, 'N', 274-418 <BOL>
A:Cross-references: UNIPARC:UP10001731BF; GB:K01396; NID:G28965
A:Note: this sequence has been corrected in reference A58528
R:Colau, B.; Chuchana, P.; Bollen, A.
DNA 3, 327-330, 1984
A:Title: Revised sequence of full-length complementary DNA coding for human alpha-1-ant
A:Reference number: A58528; MUID:8502667; PMID:6333329
A:Contents: corrections to sequence in A90944
A:Accession: A58528
A:Molecule type: mRNA
A:Residues: 1-418 <COL>
A:Cross-references: UNIPARC:UP100000CBEC; GB:K01396; NID:G28965; PIDN:CAA5838.1; PID:G
R:Ciliberto, G.; Dente, L.; Cortese, R.
Cell 41, 531-540, 1985
A:Title: Cell-specific expression of a transfected human alpha-1-antitrypsin gene.
A:Reference number: A23174; MUID:85176977; PMID:2985281
A:Accession: A23174
A:Molecule type: mRNA
A:Residues: 1-11, 13-173, 'H', 175-228, 'D', 230-418 <CIL>
A:Cross-references: UNIPARC:UP100016A3A7; GB:M11465; NID:G177826; PIDN:AA51546.1; PID:
A:Note: the authors state that this sequence corresponds to the M (normal) allele; 3 var
R:Carrell, R.W.; Jeppson, J.O.; Laurell, C.B.; Brennan, S.O.; Owen, M.C.; Vaughan, L.;
Nature 298, 339-344, 1982
A:Title: Structure and variation of human alpha-1-antitrypsin.
A:Reference number: A93281; MUID:82220135; PMID:7045697
A:Accession: A93281
A:Molecule type: protein
A:Residues: 25-418 <CAR>
A:Cross-references: UNIPARC:UP1000014E11
A:Note: peptide sequence differences with A21853 (Ileu-200 and the amidation states of re
R:Zhu, X.Y.; Kang, S.S.; Hargrove, K.; Shochat, D.; Jarrells, M.; Mojesky, M.; Chan, S.K
Biochem. J. 246, 25-36, 1987
A:Title: The identification of epitopic sites in human alpha-1-proteinase inhibitor.
A:Reference number: A32336; MUID:86049621; PMID:2445337
A:Accession: A32336
A:Molecule type: protein
A:Residues: 25-418 <ZHU>
A:Cross-references: UNIPARC:UP1000014E11
A:Note: peptides were sequenced or partially sequenced and ordered by comparison with A2
R:Weland, K.L.; Palany, C.N.; Dooley, T.P.
Submitted to the EMBL Data Library, December 1989
A:Description: Identification of a cDNA encoding a variant form of the human proteolytic

A:Reference number: S14476
A:Accession: S14476
A:Molecule type: mRNA
A:Residues: 142-230, 'Y', 232-338 <WEI>
A:Cross-references: UNIPARC:UP10000060F9; EMBL:X17122; NID:G28636; PIDN:CAA34982.1; PID
A:Experimental source: a variant form
R:Riley, J.H.; Bachurst, I.C.; Edbrooke, M.R.; Carrell, R.W.; Craig, R.K.
FEBS Lett. 189, 361-366, 1985
A:Title: Alpha-1-antitrypsin and serum albumin mRNA accumulation in normal, acute phase
A:Reference number: A24013; MUID:86005469; PMID:3876243
A:Accession: A24013
A:Molecule type: mRNA
A:Residues: 292-418 <RIL>
A:Cross-references: UNIPARC:UP1000016A3A9; EMBL:X02920; NID:G24437; PIDN:CAA26677.1; PID
R:Schulze, A.J.; Baumann, U.; Krof, S.; Jaeger, E.; Huber, R.; Laurell, C.B.
Eur. J. Biochem. 194, 51-56, 1990
A:Title: Structural transition of alpha(1)-antitrypsin by a peptide sequentially similar
A:Reference number: S13833; MUID:91071209; PMID:2253623
A:Accession: S13833
A:Molecule type: protein
A:Residues: 25-41 <SCH>
A:Cross-references: UNIPARC:UP100001731F0
R:Niemann, M.A.; Narkates, A.J.; Miller, E.J.
Matrix 12, 233-241, 1992
A:Title: Isolation and serine protease inhibitory activity of the 44-residue, C-terminal
A:Reference number: S23516; MUID:93024095; PMID:1406456
A:Accession: S23516
A:Molecule type: protein
A:Residues: 375-409, 'L', 411-413, 'S' <NIE>
A:Cross-references: UNIPARC:UP1000070F7B
R:Engler, R.; Eger, G.; Lotzspeich, F.; Plewan, A.; Ogilvie, A.; Emmerich, B.
Biol. Chem. Hoppe-Seyler 373, 581-588, 1992
A:Title: Proteolytic inactivation of alpha(1)-proteinase inhibitor in vivo: detection, c
A:Reference number: S23962; MUID:92384968; PMID:1515087
A:Accession: S23962
A:Molecule type: protein
A:Residues: 44-53, 384-392 <DEN>
A:Cross-references: UNIPARC:UP100001731F1; UNIPARC:UP100001731F2
R:Engler, R.; Lotzspeich, F.; Oberthuer, W.; Mast, A.E.; Emmerich, B.
Biol. Chem. Hoppe-Seyler 376, 165-172, 1995
A:Title: Limited proteolysis of alpha(1)-proteinase inhibitor (alpha(1)-PI) in acute leu
A:Reference number: S55249; MUID:95336645; PMID:7612193
A:Accession: S55249
A:Molecule type: protein
A:Residues: 25-28, 43-47, 207-208, 382-389, 414-418 <DS2>
A:Cross-references: UNIPARC:UP100001583FA; UNIPARC:UP100001731F3; UNIPARC:UP100001731F4;
R:Leicht, M.; Long, G.L.; Chandra, T.; Kurachi, K.; Kidd, V.J.; Mace, M.
Nature 297, 655-659, 1982
A:Title: Sequence homology and structural comparison between the chromosome human alpha
A:Reference number: I39371; MUID:82220035; PMID:6979715
A:Accession: I39371
A:Status: translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 196-225 <LEI2>
A:Cross-references: UNIPARC:UP1000016A3A6; GB:J00066; NID:G177819; PIDN:AA59370.1; PID:
R:Chang, W.S.W.; Warelle, M.R.; Lomas, D.A.; Carrell, R.W.
Biochem. J. 314, 647-653, 1996
A:Title: Probing serpin reactive-loop conformations by proteolytic cleavage.
A:Reference number: S63599; MUID:96239126; PMID:8670081
A:Accession: S63599
A:Molecule type: protein
A:Residues: 371-385 <CHA>
A:Cross-references: UNIPARC:UP100001731F7
R:Contelle, C.; Speer, A.; Rogers, J.; Kalsbeker, N.; Humphries, S.; Williamson, R.
Biomed. Biochem. Acta 44, 421-431, 1985
A:Title: Construction and partial characterization of a human liver cDNA library.
A:Reference number: I39370; MUID:85225507; PMID:3873938
A:Accession: I39370

RESULT 6
 JX0154
 alpha-1-antiprotease F - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 05-Oct-2004
 C/Accession: JX0154
 R/Saito, A.; Sinohara, H.
 J. Biochem. 109, 158-162, 1991
 A>Title: Cloning and sequencing of cDNA coding for rabbit alpha-1-antiprotease F: amir
 A/Reference number: JX0154; MUID:91201273; PMID:2016265
 A/Accession: JX0154
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-413 <SAI>
 A/Cross-references: UNIPROT:P23035; UNIPARC:UPI0000024FCB; GB:X57710; NID:g1455; PIDN:C
 C/Superfamily: serpin

Query Match 36.6%; Score 780.5; DB 2; Length 413;
 Best Local Similarity 37.5%; Pred. No. 2.3e-46;
 Matches 155; Conservative 96; Mismatches 157; Indels 5; Gaps 2;

```

QY 1 MNPTLGLAIFLAVLLTVYKGLKPSFSPRYKALSEVQGWKQMAAKELARQNMDLGFKLL 60
DB 1 MPVSVSRL---LLLAGIGCLLPGLADEAQETAVSSHEDHPACHRIAPSLAEFALSLY 57
QY 61 KCLAFYNGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPKDLHEGFHY 118
DB 58 REVAHESNTNTNIFSPVISALAFAMLSLGAAGDTHTVLEGLKFNLTETAAQIHDFGRH 117
QY 119 IIEHLQKTDODLKLSIGNTLPIDQRLQPKRFLKEDAKNPFSAETILTNFQNLMAQKQIN 178
DB 118 LHTVNRPDSELOLAAGNALVHENTLQHKFLKEDAKNLQOSEAFVDFPDPEQAKTKIN 177
QY 179 DFIQKTHGKINLNIENIDPQVWMLANYIFPRARKHEPDPVNTKEDEPLEKNSSVKY 238
DB 178 SHVEKGTGRKIVDLVQGLDARTLLALVNVYFFKGMKEPPEPENTKEEDFHVDAATTVRV 237
QY 239 PMMFRSGIYQVGYDDKLSCTILBIPYQKNTAIFILPDEGQLKLEKGLQVDTFSRKTL 298
DB 238 PMMSRLGMYVFKHCSITLSTAFVLRMDYKGNATLFLPDEGQLKLEKGLQVDTFSRKTL 297
QY 299 LSRRVVDVSPRLHMTGTFDLKKTLSYIGVKIFEEHGDITKLAHRSLSKVGSAVHRAEL 358
DB 298 SSLSRSTVHFRPKLSISGTVDLKLGLGKITQVSDNADLSGITGEQPLKASQALHRAVL 357
QY 359 KMDREGTEGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSYLFLGKIYNP 411
DB 358 TIDRGTEAAGATYMEIIPMSLPSITLDRPFLFVIYSHKISPLFVGKVVDP 410

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RESULT 7
 JX0267
 alpha-1-antiprotease S-1 precursor - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Oct-2004
 C/Accession: JX0267
 R/Saito, A.; Sinohara, H.
 J. Biochem. 113, 456-461, 1993
 A>Title: Rabbit plasma alpha-1-antiprotease s-1: cloning, sequencing, expression, and
 A/Reference number: JX0267; MUID:93293795; PMID:8514734
 A/Accession: JX0267
 A/Molecule type: mRNA
 A/Residues: 1-413 <SAI>
 A/Cross-references: UNIPROT:Q07299; UNIPARC:UPI0000086E35; GB:D16104; NID:g286191; PIDN:
 A/Experimental source: liver
 A/Note: Part of this sequence, including the amino end of the mature protein, was confir
 C/Superfamily: serpin
 C/Keywords: glycoprotein
 F.1-24/Domains: signal sequence #status predicted <SIG>
 F.25-413/Product: alpha-1-antiprotease S-1 #status experimental <MAT>
 F.65,102,266/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 36.5%; Score 778.5; DB 2; Length 413;
 Best Local Similarity 37.8%; Pred. No. 3.1e-46;
 Matches 156; Conservative 95; Mismatches 157; Indels 5; Gaps 2;

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QY 1 MNPTLGLAIFLAVLLTVYKGLKPSFSPRYKALSEVQGWKQMAAKELARQNMDLGFKLL 60
DB 1 MPVSVSRL---LLLAGIGCLLPGLADEAQETAVSSHEDHPACHRIAPSLAEFALSLY 57
QY 61 KCLAFYNGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPKDLHEGFHY 118
DB 58 REVAHESNTNTNIFSPVISALAFAMLSLGAAGDTHTVLEGLKFNLTETAAQIHDFGRH 117
QY 119 IIEHLQKTDODLKLSIGNTLPIDQRLQPKRFLKEDAKNPFSAETILTNFQNLMAQKQIN 178
DB 118 LHTVNRPDSELOLAAGNALVHENTLQHKFLKEDAKNLQOSEAFVDFPDPEQAKTKIN 177
QY 179 DFIQKTHGKINLNIENIDPQVWMLANYIFPRARKHEPDPVNTKEDEPLEKNSSVKY 238
DB 178 SHVEKGTGRKIVDLVQGLDARTLLALVNVYFFKGMKEPPEPENTKEEDFHVDAATTVRV 237
QY 239 PMMFRSGIYQVGYDDKLSCTILBIPYQKNTAIFILPDEGQLKLEKGLQVDTFSRKTL 298
DB 238 PMMSRLGMYVFKHCSITLSTAFVLRMDYKGNATLFLPDEGQLKLEKGLQVDTFSRKTL 297
QY 299 LSRRVVDVSPRLHMTGTFDLKKTLSYIGVKIFEEHGDITKLAHRSLSKVGSAVHRAEL 358
DB 298 SSRSVAVRFPKLSISGTVDLKLGLGKITQVSDNADLSGITGEQPLKASQALHRAVL 357
QY 359 KMDREGTEGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSYLFLGKIYNP 411
DB 358 TIDRGTEAAGATYVGMPSLPSISVIFDRPFLFVIYSHKISPLFVGKVVDP 410

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RESULT 8
 A54968
 alpha-1-antitrypsin precursor - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 05-Oct-2004
 C/Accession: A54968
 R/Ray, B.K.; Gao, X.; Ray, A.
 J. Biol. Chem. 269, 22080-22086, 1994
 A>Title: Expression and structural analysis of a novel highly inducible gene encoding a
 A/Reference number: A54968; MUID:94350954; PMID:8071331
 A/Accession: A54968
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-413 <RAY>
 A/Cross-references: UNIPROT:Q28666; UNIPARC:UPI00000876B0; GB:L12139; NID:g405551; PIDN:
 C/Superfamily: serpin

Query Match 36.4%; Score 775.5; DB 2; Length 413;
 Best Local Similarity 37.3%; Pred. No. 5e-46;
 Matches 154; Conservative 100; Mismatches 154; Indels 5; Gaps 2;

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QY 1 MNPTLGLAIFLAVLLTVYKGLKPSFSPRYKALSEVQGWKQMAAKELARQNMDLGFKLL 60
DB 1 MPVSVSRL---LLLAGIGCLLPGLADEAQETAVSSHEDHPACHRIAPSLAEFALSLY 57
QY 61 KCLAFYNGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQG--FNFRKMPKDLHEGFHY 118
DB 58 REVAHESNTNTNIFSPVISALAFAMLSLGAAGDTHTVLEGLKFNLTETAAQIHDFGRH 117
QY 119 IIEHLQKTDODLKLSIGNTLPIDQRLQPKRFLKEDAKNPFSAETILTNFQNLMAQKQIN 178
DB 118 LHTVNRPDSELOLAAGNALVHENTLQHKFLKEDAKNLQOSEAFVDFPDPEQAKTKIN 177
QY 179 DFIQKTHGKINLNIENIDPQVWMLANYIFPRARKHEPDPVNTKEDEPLEKNSSVKY 238
DB 178 SHVEKGTGRKIVDLVQGLDARTLLALVNVYFFKGMKEPPEPENTKEEDFHVDAATTVRV 237
QY 239 PMMFRSGIYQVGYDDKLSCTILBIPYQKNTAIFILPDEGQLKLEKGLQVDTFSRKTL 298
DB 238 PMMSRLGMYVFKHCSITLSTAFVLRMDYKGNATLFLPDEGQLKLEKGLQVDTFSRKTL 297

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QY 299 LSRVVDSVPRLLMTGTFDLKKTLSTYGVSKIFEEHGDLTAKIAPRSLKVGAVKAEI 358
 C/Spec: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
 C/Accession: I49472
 R/Borriello, F.; Krauter, K.S.
 Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
 A/Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary divergence
 A/Reference number: I49470; MUID:92052104; PMID:1946354
 A/Accession: I49470
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-413 <RES>
 A/Cross-references: UNIPROT:P07758; UNIPARC:UPI0000021A6; GB:M75721; NID:g191841; PIDN:R.Krauter, K.S.; Clifton, B.A.; Hsu, M.T.; Powell, D.; Darnell Jr., J.E.
 DNA 5, 29-36, 1986
 A/Title: Isolation and characterization of the alpha-1-antitrypsin gene of mice.
 A/Reference number: A25495; MUID:86163765; PMID:3007061
 A/Accession: A25495
 A/Molecule type: mRNA
 A/Residues: 211-245 'D', 247-322 'L', 324-403 'V', 405-413 <KRA>
 A/Cross-references: UNIPARC:UPI000016CCJ3; GB:M12586; NID:g192092; PIDN:AAA51624.1; PID: C/Genetics:
 A/Status: alpha-1 PI-1
 C/Superfamily: serpin

RESULT 9

149470
 alpha-1 proteinase inhibitor 1 - mouse
 N/Alternate names: alpha-1-antitrypsin
 C/Spec: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
 C/Accession: I49470; A25495
 R/Borriello, F.; Krauter, K.S.
 Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
 A/Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary divergence
 A/Reference number: I49470; MUID:92052104; PMID:1946354
 A/Accession: I49470
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-413 <RES>
 A/Cross-references: UNIPROT:P07758; UNIPARC:UPI0000021A6; GB:M75721; NID:g191841; PIDN:R.Krauter, K.S.; Clifton, B.A.; Hsu, M.T.; Powell, D.; Darnell Jr., J.E.
 DNA 5, 29-36, 1986
 A/Title: Isolation and characterization of the alpha-1-antitrypsin gene of mice.
 A/Reference number: A25495; MUID:86163765; PMID:3007061
 A/Accession: A25495
 A/Molecule type: mRNA
 A/Residues: 211-245 'D', 247-322 'L', 324-403 'V', 405-413 <KRA>
 A/Cross-references: UNIPARC:UPI000016CCJ3; GB:M12586; NID:g192092; PIDN:AAA51624.1; PID: C/Genetics:
 A/Status: alpha-1 PI-1
 C/Superfamily: serpin

Query Match 36.1%; Score 768.5; DB 2; Length 413;
 Best Local Similarity 39.4%; Pred. No. 1.5e-45;
 Matches 165; Conservative 85; Mismatches 158; Indels 11; Gaps 5;

QY 1 MNPTGLAIFLAVLITVKG--LKPSFSPRNKALSEVQGMKQMAKELARQNDLGRK 58
 1 MTPSISWG-----LTLAAGLCCLVPSFLAEDVQETDTSQK--DQSPASHIATNLGDFALS 54
 DB 59 LKKAFAFYNPGNRNIFLSPISITAFSMLCLGADSTLDEIKQ--FNFRKMEKDLHGEF 116
 55 LKKAFAFYNPGNRNIFLSPISITAFSMLCLGADSTLDEIKQ--FNFRKMEKDLHGEF 116
 DB 55 LKKAFAFYNPGNRNIFLSPISITAFSMLCLGADSTLDEIKQ--FNFRKMEKDLHGEF 116
 55 LKKAFAFYNPGNRNIFLSPISITAFSMLCLGADSTLDEIKQ--FNFRKMEKDLHGEF 116
 DB 117 HYIHLELQKTDKLSINTLPIQORLPORFELBDANKFYSAETILTNFQNLMAOKO 176
 115 OHILQTLNRPDSLOLSTNGFLFVNNDLKVKEFKAKNHQAEVFSVNFASEBAKV 174
 QY 177 INDPISQKHGKINNLINIDPGTMLNANYIFPRARWHEPDVNTKEDEPFLEKNSSV 236
 175 INDPISQKHGKINNLINIDPGTMLNANYIFPRARWHEPDVNTKEDEPFLEKNSSV 236
 DB 175 INDPISQKHGKINNLINIDPGTMLNANYIFPRARWHEPDVNTKEDEPFLEKNSSV 236
 175 INDPISQKHGKINNLINIDPGTMLNANYIFPRARWHEPDVNTKEDEPFLEKNSSV 236
 QY 237 KVPMMFRSGIYGVYDNDKSCITLPIYQKNTAIFILPDEGLKHLKGLQVDTFSRK 296
 235 KVPMMFRSGIYGVYDNDKSCITLPIYQKNTAIFILPDEGLKHLKGLQVDTFSRK 296
 DB 235 KVPMMFRSGIYGVYDNDKSCITLPIYQKNTAIFILPDEGLKHLKGLQVDTFSRK 296
 235 KVPMMFRSGIYGVYDNDKSCITLPIYQKNTAIFILPDEGLKHLKGLQVDTFSRK 296
 QY 297 TLLSRVVDSVPRLLMTGTFDLKKTLSTYGVSKIFEEHGDLTAKIAPRSLKVGAVK 355
 295 LKRRRLAQIHPRKLSISGEYNLKTMLSPGIRIRNAGDSLGIIEBAAPLKSQAIVK 354
 DB 355 AVLTIDETGETEAAAVTVLQVPMSPMLRPFDPFLFIIEBHQTQPIFLGKAVDPTHK 413
 356 AELKNDERTGEAAGTGAQTLPEMETPLVYKIDKPYLLIYSEKIPSVLFLGKIVNDIGK 414
 355 AVLTIDETGETEAAAVTVLQVPMSPMLRPFDPFLFIIEBHQTQPIFLGKAVDPTHK 413

RESULT 10
 149472

alpha-1 proteinase inhibitor 3 - mouse
 C/Spec: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
 C/Accession: I49472
 R/Borriello, F.; Krauter, K.S.
 Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
 A/Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary divergence
 A/Reference number: I49470; MUID:92052104; PMID:1946354
 A/Accession: I49472
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-413 <RES>
 A/Cross-references: UNIPROT:000896; UNIPARC:UPI0000028CD4; GB:M75720; NID:g191845; PIDN:J C/Genetics:
 A/Status: alpha-1 PI-3
 C/Superfamily: serpin

Query Match 36.0%; Score 766.5; DB 2; Length 413;
 Best Local Similarity 39.4%; Pred. No. 2.1e-45;
 Matches 165; Conservative 83; Mismatches 160; Indels 11; Gaps 5;

QY 1 MNPTGLAIFLAVLITVKG--LKPSFSPRNKALSEVQGMKQMAKELARQNDLGRK 58
 1 MTPSISWG-----LTLAAGLCCLVPSFLAEDVQETDTSQK--DQSPASHIATNLGDFALS 54
 DB 59 LKKAFAFYNPGNRNIFLSPISITAFSMLCLGADSTLDEIKQ--FNFRKMEKDLHGEF 116
 55 LKKAFAFYNPGNRNIFLSPISITAFSMLCLGADSTLDEIKQ--FNFRKMEKDLHGEF 116
 DB 55 LKKAFAFYNPGNRNIFLSPISITAFSMLCLGADSTLDEIKQ--FNFRKMEKDLHGEF 116
 55 LKKAFAFYNPGNRNIFLSPISITAFSMLCLGADSTLDEIKQ--FNFRKMEKDLHGEF 116
 QY 117 HYIHLELQKTDKLSINTLPIQORLPORFELBDANKFYSAETILTNFQNLMAOKO 176
 115 OHILQTLNRPDSLOLSTNGFLFVNNDLKVKEFKAKNHQAEVFSVNFASEBAKV 174
 DB 117 HYIHLELQKTDKLSINTLPIQORLPORFELBDANKFYSAETILTNFQNLMAOKO 176
 115 OHILQTLNRPDSLOLSTNGFLFVNNDLKVKEFKAKNHQAEVFSVNFASEBAKV 174
 QY 177 INDPISQKHGKINNLINIDPGTMLNANYIFPRARWHEPDVNTKEDEPFLEKNSSV 236
 175 INDPISQKHGKINNLINIDPGTMLNANYIFPRARWHEPDVNTKEDEPFLEKNSSV 236
 DB 175 INDPISQKHGKINNLINIDPGTMLNANYIFPRARWHEPDVNTKEDEPFLEKNSSV 236
 175 INDPISQKHGKINNLINIDPGTMLNANYIFPRARWHEPDVNTKEDEPFLEKNSSV 236
 QY 237 KVPMMFRSGIYGVYDNDKSCITLPIYQKNTAIFILPDEGLKHLKGLQVDTFSRK 296
 235 KVPMMFRSGIYGVYDNDKSCITLPIYQKNTAIFILPDEGLKHLKGLQVDTFSRK 296
 DB 235 KVPMMFRSGIYGVYDNDKSCITLPIYQKNTAIFILPDEGLKHLKGLQVDTFSRK 296
 235 KVPMMFRSGIYGVYDNDKSCITLPIYQKNTAIFILPDEGLKHLKGLQVDTFSRK 296
 QY 297 TLLSRVVDSVPRLLMTGTFDLKKTLSTYGVSKIFEEHGDLTAKIAPRSLKVGAVK 355
 295 LKRRRLAQIHPRKLSISGEYNLKTMLSPGIRIRNAGDSLGIIEBAAPLKSQAIVK 354
 DB 355 AVLTIDETGETEAAAVTVLQVPMSPMLRPFDPFLFIIEBHQTQPIFLGKAVDPTHK 413
 356 AELKNDERTGEAAGTGAQTLPEMETPLVYKIDKPYLLIYSEKIPSVLFLGKIVNDIGK 414
 355 AVLTIDETGETEAAAVTVLQVPMSPMLRPFDPFLFIIEBHQTQPIFLGKAVDPTHK 413

RESULT 11

149452
 alpha-1-antitrypsin precursor - mouse
 C/Spec: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
 C/Accession: I49452
 R/Sifers, R.N.; Ledley, F.D.; Reed-Fourquet, L.; Ledbetter, D.H.; Ledbetter, S.A.; Woo, S Genomics 6, 100-104, 1990
 A/Title: Complete cDNA sequence and chromosomal localization of mouse alpha-1-antitrypsin
 A/Reference number: I49452; MUID:90152670; PMID:2303252
 A/Accession: I49452
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-413 <RES>
 A/Cross-references: UNIPROT:P22599; UNIPARC:UPI0000029619; GB:M25529; NID:g191549; PIDN:J C/Superfamily: serpin

Query Match 35.7%; Score 760.5; DB 2; Length 413;
 Best Local Similarity 39.2%; Pred. No. 5.4e-45;
 Matches 165; Conservative 88; Mismatches 153; Indels 15; Gaps 7;

QY 1 MNPTGLAIFLAVLITVKG--LKPSFSPRNKALSEVQGMKQMAKELARQNDLGRK 58
 1 MTPSISWG-----LTLAAGLCCLVPSFLAEDVQETDTSQK--DQSPASHIATNLGDFALS 54

Db 1 MTPSISWG-----LILLAGLCCLVPSFLAEDVQETDTSQK-DQSPASHETATNLGDPAIS 54
Qy 59 LKKTAFAPNPGRNIFLSPLSISTASPMLCIGAODSTIDEIKQG--FNPRKMPEDIDHEGF 116
Db 55 LYRELVHQSNTSIFSPSVATATPAMLSLGSKGDTHQLLEGQFNLQTQSEADIHKSF 114
Qy 117 HYIHELTOKTODKLISGNTLPIIDORLOPQKRELEDAKNFYSAETILTNFQNLMAQKQ 176
Db 115 QHLLQTLNRPDSBLQSTGNGLFVNNDLKVEKFLBEAKNHYQAEVSVNFASEBAKAV 174
Qy 177 INDFISQKTHGKINNLIENTDPTGVTMLANTIFPRANKHEPDPNVTKEEDFLEKNSSV 236
Db 175 INDFVEKGTQKIVAEAYEILDQDTVPALGNILFKGKKKPPDEBTEBAEFHVDKSTTV 234
Qy 237 KVPMPFSGIYQVGDYDKLSTLIEIPYQKNITAFILIPDGKIKHLEKGIQVDTFSRWK 296
Db 235 KVPMTTSGMLDVHHCSTLSWVLMKDYAGNASAVFLIPBEGKQOHLEQTLNKKELIS--K 292
Qy 297 TLIS--RRVVDVSVPRILMTGTPDLKTKLSYIGYSKIPEEHGDLTKIAPHRS-LKVGSAV 353
Db 293 ILNRRRLVQIHIPRLSISGEVNLKTLMSPLGITRIFPNNGADLSGITBENAPKLKSAV 352
Qy 354 HKAKLKNDEGTGEGAAGTGAQTLPEMETPLVVKIDKPYLLILYSKIPSVLFLGKIYNPIG 413
Db 353 HKAVLTIDETGTEAATAVFEAVPMSPILRFDPHPLFIIEBHQSPIFVGKAVDPTH 412
Qy 414 K 414
Db 413 K 413

RESULT 12

149473
alpha-1 proteinase inhibitor 4 - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C/Accession: 149473
R/Bortolillo, F.; Krauter, K.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
A/Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary divergence
A/Reference number: 149470; MUID:32052104; PMID:1946354
A/Accession: 149473
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-413 <RES>
A/Cross-references: UNIPROT:Q00897; UNIPARC:UP10000003B4C; GB:M75718; NID:G191847; PIDN:
C/Genetics:
A/Gene: alpha-1 PI-4
C/Superfamily: serpin

Query Match 35.6%; Score 758.5; DB 2; Length 413;
Best Local Similarity 39.4%; Pred. No. 7.4e-45;
Matches 166; Conservative 87; Mismatches 153; Indels 15; Gaps 7;

Qy 1 MNEPLGATFLAVLITVKGH--LKPSFSPRYKALSEVQGMKQMAKELARQNMIDGFK 58
Db 1 MTPSISWG-----LILLAGLCCLVPSFLAEDVQETDTSQK-DQSPASHETATNLGDPAIR 54
Qy 59 LKKTAFAPNPGRNIFLSPLSISTASPMLCIGAODSTIDEIKQG--FNPRKMPEDIDHEGF 116
Db 55 LYRELVHQSNTSIFSPSVATATPAMLSLGSKGDTHQLLEGQFNLQTQSEADIHKSF 114
Qy 117 HYIHELTOKTODKLISGNTLPIIDORLOPQKRELEDAKNFYSAETILTNFQNLMAQKQ 176
Db 115 QHLLQTLNRPDSBLQSTGNGLFVNNDLKVEKFLBEAKNHYQAEVSVNFASEBAKAV 174
Qy 177 INDFISQKTHGKINNLIENTDPTGVTMLANTIFPRANKHEPDPNVTKEEDFLEKNSSV 236
Db 175 INDFVEKGTQKIVAEAYEILDQDTVPALGNILFKGKKKPPDEBTEBAEFHVDKSTTV 234
Qy 237 KVPMPFSGIYQVGDYDKLSTLIEIPYQKNITAFILIPDGKIKHLEKGIQVDTFSRWK 296
Db 235 KVPMTTSGMLDVHHCSTLSWVLMKDYAGNASAVFLIPBEGKQOHLEQTLNKKELISQF- 293

Qy 297 TLISRRVVD--VSVPRLMTGTPDLKTKLSYIGYSKIPEEHGDLTKIAPHRS-LKVGSAV 353
Db 294 -LNNRRSDAQIHIPRLSISGEVNLKTLMSPLGITRIFPNNGADLSGITBENAPKLKSAV 352
Qy 354 HKAKLKNDEGTGEGAAGTGAQTLPEMETPLVVKIDKPYLLILYSKIPSVLFLGKIYNPIG 413
Db 353 HKAVLTIDETGTEAATAVQVATYSPPIYRFPHPFLFIIEBHQSPIFVGKAVDPTH 412
Qy 414 K 414
Db 413 K 413

RESULT 13

149471
alpha-1 proteinase inhibitor 2 - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
C/Accession: 149471
R/Bortolillo, F.; Krauter, K.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
A/Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary divergence
A/Reference number: 149470; MUID:32052104; PMID:1946354
A/Accession: 149471
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-402 <RES>
A/Cross-references: UNIPROT:P22599; UNIPARC:UP1000016CBEA; GB:M75716; NID:G191843; PIDN:
C/Genetics:
A/Gene: alpha-1 PI-2
C/Superfamily: serpin

Query Match 35.5%; Score 756; DB 2; Length 402;
Best Local Similarity 40.1%; Pred. No. 1.1e-44;
Matches 159; Conservative 85; Mismatches 145; Indels 8; Gaps 5;

Qy 23 PSFSPRYKALSEVQGMKQMAKELARQNMIDGFKLKKLAFNPGRNIFLSPLSISTA 82
Db 9 PSFLAEDVQETDTSQK-DQSPASHETATNLGDPAISLYRELVHQSNTSIFSPSVATATA 67
Qy 83 FSNLCIGAODSTIDEIKQG--FNPRKMPEDIDHEGFYIHELTOKTODKLISGNTLFI 140
Db 68 FANLSLGSKGDTHQLLEGQFNLQTQSEADIHKSFQHLQTLNRPDSBLQSTGNGLFV 127
Qy 141 DQRLQPKRELEDAKNFYSAETILTNFQNLMAQKQINDFISQKTHGKINNLIENTDPT 200
Db 128 NNDLKVEKFLBEAKNHYQAEVSVNFASEBAKAVINDFVEKGTQKIVAEAYEILDQDT 187
Qy 201 VMLANTIFPRANKHEPDPNVTKEEDFLEKNSSVYKPMFSGIYQVGDYDKLSTIL 260
Db 188 VPALANTIFPKGKKKPPDEBTEBAEFHVDKSTTVAVPMMLSGMLDVHHCSTLSWV 247
Qy 261 EIPYQKNITAFILIPDGKIKHLEKGIQVDTFSRWKTLIS--RRVVDVSVPRILMTGTPD 318
Db 248 LMDYAGNASAVFLIPBEGKQOHLEQTLNKKELIS--KILNRRRLVQIHIPRLSISDYN 305
Qy 319 LKKTLSYIGYSKIPEEHGDLTKIAPHRS-LKVGSAVHKAELKNDEGTGEGAAGTGLP 377
Db 306 LKTLMSPLGITRIFPNNGADLSGITBENAPKLKSAVHKAVALTIDETGTEAATAVFEAVP 365
Qy 378 METPLVVKIDKPYLLILYSKIPSVLFLGKIYNPICK 414
Db 366 MSMPILRFDPHPLFIIEBHQSPIFVGKAVDPTHK 402

RESULT 14

S60036
alpha-1-antitrypsin precursor - golden hamster
N/Alternate names: alpha-1-antitrypsinase
C/Species: Mesocricetus auratus (golden hamster)
C/Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 05-Oct-2004
C/Accession: S60036

R:Nakatsuji, T.; Suzuki, Y.; Yoshida, K.; Shinohara, H.
 Blochm. Blochm. Acta 1263, 245-248, 1995
 A>Title: Molecular cloning and sequence analysis of cDNA encoding plasma alpha-1-antitrypsin
 A:Reference number: S60036; MID:96004896; PMID:7548212
 A:Accession: S60036
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-413 <NA>
 A:Cross-references: UNIPROT:P92727; UNIPARC:UPI0000067E5; EMBL:D49709; NID:G1088432; PI
 A>Note: the source is designated as Syrian hamster
 C:Superfamily: serpin
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-413/Product: alpha-1-antitrypsin #status predicted <MAT>

Query Match 35.4%; Score 753; DB 2; Length 413;
 Best Local Similarity 38.7%; Pred. No. 1,8e-44;
 Matches 161; Conservative 87; Mismatches 158; Indels 10; Gaps 4;

QY 1 MNPTGLAIFLAVLLTVKGL--LKPSPPNNYKALSEVQGMKQMAKELARQNMDLGFK 58
 DB 1 MKPSISMGILL-----LAGLCLVPSFLAEDAQETDASKQDQHQAACKIAPNLADFSFN 55

QY 59 LKGLAFNPGRIIFSLPISITAFSMCLGADSTLDEIKQ--GRYFRKMPKEDLHEGF 116
 DB 56 LKRELHQSNTTNIIFSPSIAIAFAMLSIGTKVHTTQILEGLFNLTEIAAEVHKGK 115

QY 117 HYIHIELTQKTDLKLISGNTLFIIDRLQPORKELEDKAFSAETILTNPONLEMAQK 176
 DB 116 HNLLQTFNRPDNELOLTGNGLFTHNNLKYDKEBEVKNQDYSSEAFVNFTSSEAKKY 175

QY 177 INDFISQKTHGKINNLINENIDPGTMLANYIFFPRAWKHEFDPNVTKBEDPFLERKSSV 236
 DB 176 INGFEVKGTOGKIVDLVKDLKDQTVLALVYIIFPKGKMKKPFADNTEADPFVADKTTYV 235

QY 237 KYPMFMRSGIYQGVGDKSCITLLEIPYQKNITAFILPDEGLKHLKGLQVDTFSRK 296
 DB 236 KQPMMSRLMFPDHYVSTLSSVWLLMDYLGNAATAFILPDGKQHLBQTLNKEITIGKFL 295

QY 297 TLISRAVVDVSVRLMTGTFDLKKTLSTYIGVSKIPEEHGDLTKIAPHRSLKVGSAVHKA 356
 DB 296 KDRHRSAAVHPPKLSISGYNKLALDPLGITOVFSNGADLSGITEDVPLKGLKAVHKA 355

QY 357 ELKMDERTGGAAGTGAQTLPMETPLVVKIDKPYLLIYS-EKIPSVLFLGKIIVP 411
 DB 356 VLTIDERTGAAGATFMEITIPMSVPEVNFNSPFIATIIDYDQAKSPLFVGKVVDP 411

RESULT 15

S11320
 aerine protease inhibitor 3 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-Oct-2004
 C:Accession: S11320; S08100
 R:Pages, G.; Rouayenc, U.F.; le Cam, G.; Mariller, M.; le Cam, A.
 Eur. J. Biochem. 190, 385-391, 1990
 A>Title: Molecular characterization of three rat liver serine-protease inhibitors affect
 A:Reference number: S11318; MID:90306038; PMID:1694763
 A:Accession: S11320
 A:Molecule type: mRNA
 A:Residues: 1-408 <PAG>
 A:Cross-references: UNIPARC:UPI0000167956; EMBL:X16359; NID:G57234; PTDN:CA34408.1; PID
 R:le Cam, A.
 submitted to the EMBL Data Library, August 1989
 A:Reference number: S08099
 A:Accession: S08100
 A:Molecule type: mRNA
 A:Residues: 1-366 <LBC>
 A:Cross-references: UNIPARC:UPI0000176300; EMBL:X16359
 C:Superfamily: serpin

Query Match 35.1%; Score 747.5; DB 2; Length 408;
 Best Local Similarity 40.6%; Pred. No. 4.2e-44;
 Matches 151; Conservative 79; Mismatches 133; Indels 9; Gaps 5;

QY 48 LARQNMDLGFKLKLAFNPGRIIFSLPISITAFSMCLGADSTLDEIKQ--FNFR 105
 DB 37 LMSINDPFAFSLYKGLALNPNHNVVPSLISALAAVSLGAKSGSMEEILGLKFNLT 96

QY 106 KPEKDLHGFHYIHELTOKTDLKLISGNTLFIIDRLQPORKELEDKAFSAETILT 165
 DB 97 EYFETRIHGFHGLIQLRSLQPRDEIQISTGNALFIEKRLQVLAEPQEKAKALYQAEAFYA 156

QY 166 NPNLEMAQKQINDFISQKTHGKINNLINENIDPGTMLANYIFFPRAWKHEFDPNVTKG 225
 DB 157 DFOQSRKAKLLINDVSKOTQKIQGLITNLAKKISMWLVNVIYFGKMKVPPDPDPTQ 216

QY 226 EDFLEKNSVYKPMFRSGIYQGV--DDKLSCTTLEIPYQKNITAFILPDEGLKHL 283
 DB 217 SEFYSGKRSSVYKPMFKLEDL--TTPYVRDEELNCTVLELKTGNASALFILPDQGMQV 275

QY 284 EKGQVDTFSRMKTLISRAVVD--VSVRLMTGTFDLKKTLSTYIGVSKIPEEHGDLTKIA 342
 DB 276 EASLOPETLRRWKDSIRPSPMIDELYLPKFSISADVNLBDVLPELGKEVFSQADLSGIT 335

QY 343 PHRSLLKVGSAVHKAELKMDERTGGAAGTGAQTLPMET--PLVVKIDKPYLLIYSEKI 399
 DB 336 GKDQLNVQVHKAVDVAETGEAATAVGKVPKSAKLDPILIAFDPPMLITSDTER 395

QY 400 PSVLFGLKIIVP 411
 DB 396 ALAPFLAKIFNP 407

Search completed: March 31, 2006, 09:50:51
 Job time : 42 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 31, 2006, 09:43:04 ; Search time 233 Seconds
(without alignments)
1253.600 Million cell updates/sec

Title: US-10-664-356-1562

Perfect score: 2130
Sequence: 1 MNPTGLAIFLAVLLTVKGL.....YSEKIPSVLFLGIKIVNPIGK 414

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:.*
1: uniprot_sprotc:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2130	100.0	414	2 Q81W75	HOMO SAPIEN
2	1406	66.0	411	2 Q8R421	RAT
3	1380	64.8	413	2 Q7JMF5	MOUSE
4	1378	64.7	413	2 Q9C032	MOUSE
5	1369	64.3	413	2 Q6P6M3	MOUSE
6	876.5	41.2	432	2 Q6STX0	XENLA
7	857	40.2	431	2 Q6KXK6	XENLA
8	857	40.2	433	2 Q9Y1B8	XENLA
9	841	39.5	436	2 Q5M911	XENTR
10	827	38.8	426	2 Q8JTA6	SPHPU
11	792	37.2	396	1 A1AT_C6RAB	
12	790	37.1	418	1 A1AT_PONPY	
13	787	36.9	409	1 A1AT_PAPAN	
14	785.5	36.9	413	2 Q28665	RABIT
15	785	36.9	411	1 A1AT_RAT	
16	785	36.9	418	1 A1AT_HUMAN	
17	785	36.9	418	2 Q53XB8	HUMAN
18	782	36.7	406	1 A1AT_MERUN	
19	780.5	36.6	413	1 A1AT_RABIT	
20	778.5	36.5	413	2 Q07298	RABIT
21	775.5	36.4	413	2 Q28666	RABIT
22	772.5	36.3	456	2 Q62663	RABIT
23	772	36.2	411	2 Q9TPE1	BOVIN
24	768.5	36.1	413	1 A1AT1_MOUSE	
25	766.5	36.0	413	1 A1AT3_MOUSE	
26	766	35.9	417	2 Q5J801	BOVIN
27	764	35.8	415	2 Q9GMA6	PIG
28	763	35.8	421	1 A1AT_PIG	
29	762.5	35.8	413	1 A1AT2_MOUSE	
30	761	35.7	412	1 A1AT_CALCAN	
31	758.5	35.6	413	1 A1AT_MOUSE	

32	753	35.4	413	1 A1AT_MESAU	P97277 mesocricetu
33	752.5	35.3	412	1 A1AT2_MOUSE	P81105 mus musculus
34	752.5	35.3	420	2 Q60552	MESAU
35	752	35.3	421	1 A1AT2_HORSE	Q60552 mesocricetu
36	745.5	35.0	413	2 Q8VC41	MESAU
37	745	35.0	413	1 CP13_RAT	P38029 equus caball
38	743.5	34.9	418	1 CP16_RAT	Q8VC41 mus musculus
39	742.5	34.9	413	1 A1AT5_MOUSE	P05544 rattus norv
40	742.5	34.9	413	2 Q545P1	MESAU
41	742	34.8	416	1 A1AT_BOVIN	Q00898 mus musculus
42	740	34.7	413	1 ALMS_SPEPR	Q545P1 mus musculus
43	737.5	34.6	416	1 CP11_RAT	P34955 bos taurus
44	735	34.5	445	1 SP43F_MOUSE	O54761 spermophilu
45	733	34.4	413	2 Q76HP0_TAMSI	P05545 r contrapeti
					Q80X76 mus musculus
					Q76HP0 tamias sibi

ALIGNMENTS

RESULT 1
Q81W75 HUMAN PRELIMINARY; PRT; 414 AA.
AC Q81W75;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Serine (or cysteine) proteinase inhibitor, clade A (Alpha-1
DE antiprotease, antitrypsin), member 12 (OL-64) (Visceral adipose-
DE specific SERPIN).
GN Name=SERPINA12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
CX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Helte F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshimuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka J., Smallie D.E.,
RA Schnerbach A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RG NIH MGC Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RA Chen S., Guo J.H., Yu L.,
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Hida K., Wada J., Zhang H.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

-1- SIMILARITY: Belongs to the serpin family.
 CC EMBL: BC040857, AA040857.1; -; mRNA.
 DR EMBL: AY177692, AA018649.1; -; mRNA.
 DR EMBL: AY326420, AAP89384.1; -; mRNA.
 DR HSSP: P01009; 10MB.
 DR Ensembl: ENSG00000065953; Homo sapiens.
 DR HGNC: HGNC:18359; SERPIN12.
 DR GO: GO:0004867; F-serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro: IPR000215; Prot_inh_serpin.
 DR Pfam: PF00079; Serpin; 1.
 DR SMART: SM00093; SERPIN; 1.
 KM Serpin.
 SQ SEQUENCE 414 AA; 47175 MW; 5C70F1AB5935661C CRC64;
 Query Match 100.0%; Score 2130; DB 2; Length 414;
 Best Local Similarity 100.0%; Pred. No. 2,3e-143;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNPTGLAIFLAVLLTVKGLIKPSFSPRNKALSEVQGMKQMAAKELARQNDLGFKLL 60
 DB 1 MNPTGLAIFLAVLLTVKGLIKPSFSPRNKALSEVQGMKQMAAKELARQNDLGFKLL 60
 QY 61 KGLAFNPGRNIFLSPLSISTAFSMCLGADSTLDEIKQFNFRKMPKEDLHEGFHYII 120
 DB 61 KGLAFNPGRNIFLSPLSISTAFSMCLGADSTLDEIKQFNFRKMPKEDLHEGFHYII 120
 QY 121 HELTQTDKLKLSIGNTLFIQRLQFORKFLBDANKFYSAETILTNFQNLMAQKQINDF 180
 DB 121 HELTQTDKLKLSIGNTLFIQRLQFORKFLBDANKFYSAETILTNFQNLMAQKQINDF 180
 QY 181 ISQKTHGKINNTLENIIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVM 240
 DB 181 ISQKTHGKINNTLENIIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVM 240
 QY 181 ISQKTHGKINNTLENIIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVM 240
 DB 181 ISQKTHGKINNTLENIIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVM 240
 QY 241 MFRSGIYGVYGDKLSCTLLEIPYQKNITAFILPDEGKIKLKEGLQVDTFSRMKTLIS 300
 DB 241 MFRSGIYGVYGDKLSCTLLEIPYQKNITAFILPDEGKIKLKEGLQVDTFSRMKTLIS 300
 QY 301 RRVDVSVRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTFLAPRSLKYGEAVHKAELKM 360
 DB 301 RRVDVSVRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTFLAPRSLKYGEAVHKAELKM 360
 QY 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLKQVNPICK 414
 DB 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLKQVNPICK 414
 RESULT 2
 Q8R4Z1_RAT PRELIMINARY; PRT; 411 AA.
 ID Q8R4Z1;
 AC Q8R4Z1;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Visceral adipose tissue specific SERPIN.
 GN Name=Serpin12; Synonyms=Vaepin;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OK NCBI_TaxId=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=OLETF; TISSUE=Visceral adipose;
 RA Hida K., Wada J., Zhang H., Shikata K., Makino H.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBD databases.
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL: AF245398, AAL95574.1; -; mRNA.
 DR HSSP: P01008; 1ATN.
 DR Ensembl: ENSRNOG0000009710; Rattus norvegicus.
 DR RGD: 708485; Serpin12.
 DR GO: GO:0004867; F-serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro: IPR000295; Prot_inh_serp2.

InterPro: IPR000215; Prot_inh_serpin.
 DR Pfam: PF00079; Serpin; 1.
 DR PRINTS: PR00780; LEUSERPINII.
 DR SMART: SM00093; SERPIN; 1.
 KM Serpin.
 SQ SEQUENCE 411 AA; 47527 MW; 29FA271FP8CC8A2D CRC64;
 Query Match 66.0%; Score 1406; DB 2; Length 411;
 Best Local Similarity 62.8%; Pred. No. 8.8e-92;
 Matches 258; Conservative 84; Mismatches 69; Indels 0; Gaps 0;
 QY 1 MNPTGLAIFLAVLLTVKGLIKPSFSPRNKALSEVQGMKQMAAKELARQNDLGFKLL 60
 DB 1 MNPTGLAIFLAVLLTVKGLIKPSFSPRNKALSEVQGMKQMAAKELARQNDLGFKLL 60
 QY 61 KGLAFNPGRNIFLSPLSISTAFSMCLGADSTLDEIKQFNFRKMPKEDLHEGFHYII 120
 DB 61 KGLAFNPGRNIFLSPLSISTAFSMCLGADSTLDEIKQFNFRKMPKEDLHEGFHYII 120
 QY 121 HELTQTDKLKLSIGNTLFIQRLQFORKFLBDANKFYSAETILTNFQNLMAQKQINDF 180
 DB 121 HELTQTDKLKLSIGNTLFIQRLQFORKFLBDANKFYSAETILTNFQNLMAQKQINDF 180
 QY 181 ISQKTHGKINNTLENIIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVM 240
 DB 181 ISQKTHGKINNTLENIIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVM 240
 QY 181 ISQKTHGKINNTLENIIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVM 240
 DB 181 ISQKTHGKINNTLENIIDPGTMLLANYIFPRARKHEPDNVTKEEDFLEKNSVYKVM 240
 QY 241 MFRSGIYGVYGDKLSCTLLEIPYQKNITAFILPDEGKIKLKEGLQVDTFSRMKTLIS 300
 DB 241 MFRSGIYGVYGDKLSCTLLEIPYQKNITAFILPDEGKIKLKEGLQVDTFSRMKTLIS 300
 QY 301 RRVDVSVRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTFLAPRSLKYGEAVHKAELKM 360
 DB 301 RRVDVSVRLHMTGTFDLKKTLSYIGVSKIFEEHGDLTFLAPRSLKYGEAVHKAELKM 360
 QY 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLKQVNPICK 411
 DB 361 DERGTGAAGTGAQTLPMTPLVVKIDKPYLLIYSEKIPSVLFLKQVNPICK 411
 RESULT 3
 Q7TMP5_MOUSE PRELIMINARY; PRT; 413 AA.
 ID Q7TMP5;
 AC Q7TMP5;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Visceral adipose-specific SERPIN.
 GN Name=Serpin12;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OK NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Swiss Webster;
 RA Hida K., Wada J., Zhang H.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBD databases.
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL: AY326419, AAP88383.1; -; mRNA.
 DR HSSP: P01008; 1ATN.
 DR MGI: MGI:1915304; Serpin12.
 DR GO: GO:0005615; C-extracellular space; TAS.
 DR InterPro: IPR000295; Prot_inh_serp2.
 DR InterPro: IPR000215; Prot_inh_serpin.
 DR Pfam: PF00079; Serpin; 1.
 DR PRINTS: PR00780; LEUSERPINII.
 DR SMART: SM00093; SERPIN; 1.
 DR PROSITE: PS00284; SERPIN; 1.
 KM Serpin.
 SQ SEQUENCE 413 AA; 47674 MW; E52B3B08C2DD418F CRC64;

Query Match 64.8%; Score 1380; DB 2; Length 413;
 Best Local Similarity 61.3%; Pred. No. 6.3e-90;
 Matches 253; Conservative 85; Mismatches 75; Indels 0; Gaps 0;

QY 1 MNPFLGALPLAVLITTKGKLFSPRYKALSEVQGMKORMAKELARONDLGRFL 60
 DB 1 MTRMLDGLPLAGLLTVKGLLQDDADAPMDSPRVQVEMRGKQARQLARINMEGFRL 60
 QY 61 KKLAFYNGNNIFLPSLSTAFPSMLCLGADSTLDELKOGFNPRKBEKHLGHPYII 120
 DB 61 QRLASNSPRGNIFLPSLSTAFPSMLCLGADSTLDELKOGFNPRKBEKHLGHPYII 120
 QY 121 HELTQTKDGLKLSGNTLFTDQLQPKFLKEDAKNFYSATLITLNFONLEMAKQINDF 180
 DB 121 HKLQNETEDTKMGNLFPMDQKLRPOORFLNLAKNVYDADMDVLTINQDLENTKQINDRY 180
 QY 121 ISQTKHKKINLLENIDPRGYMLANTIFPRAKKHEPDNPVTKEDPFLKNSVYVPM 240
 DB 181 ISRTSHRIKMWVSIDPGVTMLTNYIFRGWQYFDPKQTEBEPFTEKGTIVVPM 240
 QY 241 MPRSGIYQVGYDDKLSCTILEIPYOKNITAFILPDGSKLKHLEKGLQVDPFSRWKTL 300
 DB 241 MPRGGLYDAMVDSQLSTLIEIPRGKITVLPDNGKLLKLGQGLQDIFAKWKSLLS 300
 QY 301 RRVVDSVPLHMTGTFDKLTKLSTYIGSVKIFEBHGDLTAKIAPRSLKVGSAVAKELKM 360
 DB 301 KRVVDVWVPLRISSTYTNMKKVLRLGISKIFENGDLTSHSRSLKVGSAVAKELKM 360
 QY 361 DEGTGCACTGAGTLPMTPLVYKIDKPYLLISKIRSVLFLGIYVPIG 413
 DB 361 DEKGMEGAAGSAGTLPMTPLRHKLDRLPFLMIYENFMPSMIFLARIYDPSG 413

RESULT 4
 Q9C032 MOUSE PRELIMINARY; PRT; 413 AA.

ID Q9C032; 01-JUN-2001 (TrEMBLrel. 17, Created)
 AC Q9C032; 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched
 DE library, clone:4632419J12 product:hypothetical Serpins containing
 DE protein, full insert sequence (Mus musculus 17 days embryo head cDNA,
 DE RIKEN full-length enriched library, clone:3300001F13
 DE product:hypothetical Serpins containing protein, full insert
 DE sequence).
 GN Name=Serpina12;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Izawa K., Nishi K., Kiyosawa H., Kondo S., Yamakawa I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Scudliff F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustlisch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima M., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker G., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Oshio N., Saito R., Suzuki H., Yamakawa I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schoenbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Choithia C., Corbani L.B., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustlisch S., Hirokawa N., Jackson I.D., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sample C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Wetlande J., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Izawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai D., Shibata K., Shinagawa A.,
 RA Yuenishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:11617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Izawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Katsunari T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaishvagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
 RA Adachi J., Izawa K., Akiyama T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurthara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito R., Saito C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.,
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL: AK014589; BAB29447.1; -; mRNA.
 DR EMBL: AK014346; BAB29287.1; -; mRNA.
 DR HSSP: P01008; IATH.
 DR Ensemble: ENSMUSG0000041567; Mus musculus.
 DR MGI: MGI:1915304; Serpin12.
 DR GO: GO:0005615; Extracellular space; TAS.
 DR InterPro: IPR000295; Prot_inh_Lserp2.
 DR InterPro: IPR000215; Prot_inh_serpin.
 DR Pfam: PF00079; Serpin_1.
 DR PRINTS: PR00780; LEUSERPIN1.
 DR SMART: SM00093; SERPIN; 1.
 DR PROSITE: PS00284; SERPIN; 1.
 DR Hypothetical protein; Serpin.
 KW SEQUENCE 413 AA; 47634 MW; D0A8E1BE24FD60A CRC64;

Query Match 64.7%; Score 1378; DB 2; Length 413;
 Best Local Similarity 61.5%; Pred. No. 8, 8e-90;
 Matches 254; Conservative 83; Mismatches 76; Indels 0; Gaps 0;

QY 1 MNPFTGLAFLAVLTIVYGLKSPSPRYKALSVQCKQKMAKELARQNMDELGFLL 60
 DB 1 MTRMLDLGLFPGLLTVKGLQDRDAPDMYDSVPRVQEWGRKQDAQLARHNMEEFGFKLL 60
 QY 61 KKLAFYNGRNIFLSPISISTAFSMCLGADSTLDEIKQGFNRKPEKDLHEGFHYII 120
 DB 61 QRLAANSRGNIFLSPISISTAFSMCLGADSTLDEIKQGFNRKPEKMSWDVHAHFHYLL 120
 QY 121 HELYQKTDCLKISGNTLPIIDRLQOPQKFLBDANKFYSAETILTNFQNLMAQKQINDF 180
 DB 121 HKLANQETEDTKMNLGNALFMQDKLRPQORFLNLAQNVVDADWVLTNFDLENTQKQINDRY 180
 QY 181 ISQKTHGKINNLINENIDPQTNMLNANYIFPRARKHGERPNTYKEDPFLEKSSVKKVPM 240
 DB 181 ISQKTHSRKKNWKSIDPQTNMLNANYIFPRGRWQEPDPQKTEEFIEKQKTVKVPW 240
 QY 241 MFRSGIYGVYDDKLSCTILIEIPYQKNITAFILPDEGKLKHLKGLQVDFSRMKTLLS 300
 DB 241 MFGRLYDMAVDSQSCTILIEIPYQKNITAFILPDEGKLKHLKGLQVDFSRMKTLLS 300
 QY 301 RRVDVSVPRLMHTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSLVGEAVHKAELKM 360
 DB 301 KRVDVWVWPKLRISSTYNNKKVLSRLGISKIFEEHNDLTRISSHRSKLVGEAVHKAELKM 360
 QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSYLFLGKIVNPIG 413
 DB 361 DEKGMEGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSYLFLGKIVNPIG 413

RESULT 5

O6P6M3 MOUSE

ID O6P6M3_MOUSE PRELIMINARY; PRT; 413 AA.

AC O6P6M3,
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Visceral adipose-specific SERPIN.
 GN Name=Serpin12;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OC NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=aw and limb;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Steinberg R.L., Felngold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shemen C.M., Schler G.D.,
 RA Altshuler R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usslin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.U., Malek J.A., Gnatratne P.H.,
 RA Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield J.S.N., Krzywinski M.I., Skalska U., Smaliv D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=aw and limb;
 RG NIH MGC Project;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL: BC062143; AAH62143.1; -; mRNA.
 DR HSSP: P01008; IATH.
 DR Ensemble: ENSMUSG0000041567; Mus musculus.
 DR MGI: MGI:1915304; Serpin12.
 DR GO: GO:0005615; Extracellular space; TAS.
 DR InterPro: IPR000295; Prot_inh_Lserp2.
 DR InterPro: IPR000215; Prot_inh_serpin.
 DR Pfam: PF00079; Serpin_1.
 DR PRINTS: PR00780; LEUSERPIN1.
 DR SMART: SM00093; SERPIN; 1.
 DR PROSITE: PS00284; SERPIN; UNKNOWN_1.
 KW Serpin.
 SQ SEQUENCE 413 AA; 47630 MW; CE1940BA2E35811 CRC64;

Query Match 64.3%; Score 1369; DB 2; Length 413;
 Best Local Similarity 60.5%; Pred. No. 3, 8e-89;
 Matches 250; Conservative 87; Mismatches 76; Indels 0; Gaps 0;

QY 1 MNPFTGLAFLAVLTIVYGLKSPSPRYKALSVQCKQKMAKELARQNMDELGFLL 60
 DB 1 MTRMLDLGLFPGLLTVKGLQDRDAPDMYDSVPRVQEWGRKQDAQLARHNMEEFGFKLL 60
 QY 61 KKLAFYNGRNIFLSPISISTAFSMCLGADSTLDEIKQGFNRKPEKDLHEGFHYII 120
 DB 61 QRLAANSRGNIFLSPISISTAFSMCLGADSTLDEIKQGFNRKPEKMSWDVHAHFHYLL 120
 QY 121 HELYQKTDCLKISGNTLPIIDRLQOPQKFLBDANKFYSAETILTNFQNLMAQKQINDF 180
 DB 121 HKLANQETEDTKMNLGNALFMQDKLRPQORFLNLAQNVVDADWVLTNFDLENTQKQINDRY 180
 QY 181 ISQKTHGKINNLINENIDPQTNMLNANYIFPRARKHGERPNTYKEDPFLEKSSVKKVPM 240
 DB 181 ISKTHSRKKNWKSIDPQTNMLNANYIFPRGRWQEPDPQKTEEFIEKQKTVKVPW 240
 QY 241 MFRSGIYGVYDDKLSCTILIEIPYQKNITAFILPDEGKLKHLKGLQVDFSRMKTLLS 300
 DB 241 MFGRLYDMAVDSQSCTILIEIPYQKNITAFILPDEGKLKHLKGLQVDFSRMKTLLS 300
 QY 301 RRVDVSVPRLMHTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSLVGEAVHKAELKM 360
 DB 301 KRVDVWVWPKLRISSTYNNKKVLSRLGISKIFEEHNDLTRISSHRSKLVGEAVHKAELKM 360
 QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSYLFLGKIVNPIG 413
 DB 361 DEKGMEGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSYLFLGKIVNPIG 413

RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL: BC078523; AA078523.1; -, mRNA.
 DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro: IPR000295; Prot_inh_serpin.
 DR InterPro: IPR000215; Prot_inh_serpin.
 DR Pfam: PF00079; Serpin_1.
 DR PRINTS: PR00780; LEUSERPIN1.
 DR SMART: SM00093; SERPIN_1.
 DR PROSITE: PS00284; SERPIN; 1.
 DR Serpin.
 KW Serpin.
 SQ SEQUENCE 431 AA; 48870 MW; 41ADE4EC6B8ED57 CRC64;
 Query Match 40.2%; Score 857; DB 2; Length 431;
 Best Local Similarity 42.6%; Pred. No. 1.3e-52;
 Matches 159; Conservative 91; Mismatches 121; Indels 2; Gaps 1;
 QY 41 ORMAAKELARONNDLGFLLKLLAFYNGRNIFLSPISITAFSMCLGADSTLDEIKQ 100
 DB 57 ESMPCIKIAPRYNAHFPSLYRKLAADNPTENIFLSPVISITAFAMLSLGAQGLNQIYE 116
 QY 101 G--FNRKMPKEDLHGFFHYIHELTOQTODKLSTIGNTLFTIDRLQPKRFLDANKFY 158
 DB 117 GLSFNTTEISEEIHKGFOHLMLNDPSEMGNLGMLFIDKDPQIIQKFLVDKQFY 176
 QY 159 SAEITLTNQNLMAOKQINDPISQTKGKINNLINIDPGVMTLANTYFFRAWKHF 218
 DB 177 EAEPSSTDHNTBEAKQINSYAEKKTNGKITELSTVDEKTLVINYIYFRGWKEKPF 236
 QY 219 DPNVTEKEDPFLKSNSSVYPMWFRSGIYQVGYDDKLSCTIIEIPYOKNTAIFILPDG 278
 DB 237 EKENTVDGEFHYDQVTVVYPMHKGKMTNVAYDDQGLCTVLMFPGKNAITAFILPDG 296
 QY 279 KKLHLEKGLQVDTFSRKMTLLSRVVDVSPRLMTGTFDLKKTLSTYIGVSKIPEEHGDL 338
 DB 297 KLRQVEALELTPVVKSMRKIFRRRSVNLTPKFSISATLDLVKELRGVTDVFSGSMNL 356
 QY 339 TKIAPHRSLKVGAEVAKELKNDERTGEGAGTGLPMETPLVVKIDKPYLLIYSK 398
 DB 357 SGITEAPPLRVSAVKAVALSIDETGETEAGVGMELPMWVSRIEFNKPFLIITYGQ 416
 QY 399 IPSVLPFLGIKINP 411
 DB 417 TRSNYFMGRINMP 429
 RESULT 8
 QYI1B8 XENLA PRELIMINARY; PRT; 433 AA.
 AC 09YI1B8;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alpha-1-antitrypsinase.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 NCBI_TaxID=8355;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=liver;
 RA Yoshida K., Suzuki Y., Sinohara H.;
 RT "Cloning and comparative sequence analysis of Xenopus laevis alpha1-
 RT antitrypsinase."
 RL J. Biochem. Mol. Biol. Biophys. 3:59-63(1999).
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL: AB014091; BAA36581.1; -, mRNA.
 DR HSPF; P01009; IOMB.

DR GO: GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro: IPR000295; Prot_inh_serpin.
 DR InterPro: IPR000215; Prot_inh_serpin.
 DR Pfam: PF00079; Serpin_1.
 DR PRINTS: PR00780; LEUSERPIN1.
 DR SMART: SM00093; SERPIN_1.
 DR PROSITE: PS00284; SERPIN; UNKNOWN_1.
 DR Serpin.
 KW Serpin.
 SQ SEQUENCE 433 AA; 48909 MW; 4E37C65317BCF2AC CRC64;
 Query Match 40.2%; Score 857; DB 2; Length 433;
 Best Local Similarity 42.6%; Pred. No. 1.3e-52;
 Matches 159; Conservative 87; Mismatches 125; Indels 2; Gaps 1;
 QY 41 ORMAAKELARONNDLGFLLKLLAFYNGRNIFLSPISITAFSMCLGADSTLDEIKQ 100
 DB 59 ESMPCIKIAPRYNAHFPSLYRKLAADNPTENIFLSPVISITAFAMLSLGAQGLNQIYE 118
 QY 101 G--FNRKMPKEDLHGFFHYIHELTOQTODKLSTIGNTLFTIDRLQPKRFLDANKFY 158
 DB 119 GLSFNTTEISEEIHKGFOHLMLNDPSEMGNLGMLFIRNNKLQKFLVDKQIY 178
 QY 159 SAEITLTNQNLMAOKQINDPISQTKGKINNLINIDPGVMTLANTYFFRAWKHF 218
 DB 179 GSEAFSTDHNTBEAKQINSYAEKKTNGKITELSTVDEKTLVINYIYFRGWKEKPF 238
 QY 219 DPNVTEKEDPFLKSNSSVYPMWFRSGIYQVGYDDKLSCTIIEIPYOKNTAIFILPDG 278
 DB 239 DEELTQDGIFFYDENTNTVYPMHKGKMTNVAFDKGLCTVQIIPKGNASALFILPDG 298
 QY 279 KKLHLEKGLQVDTFSRKMTLLSRVVDVSPRLMTGTFDLKKTLSTYIGVSKIPEEHGDL 338
 DB 299 KLRQVEALELTPVVKSMRKIFRYQSVRLSIPKFSISAEIDLIEVFKGLGVTDFVSEADL 358
 QY 339 TKIAPHRSLKVGAEVAKELKNDERTGEGAGTGLPMETPLVVKIDKPYLLIYSK 398
 DB 359 TGIVEAKKLKVAHKAVALSIDETGETEAAATFAEIMPMPLPNTQYRPLTIYDWE 418
 QY 399 IPSVLPFLGIKINP 411
 DB 419 TKGHTLFLGRINMP 431
 RESULT 9
 QSM911 XENTR PRELIMINARY; PRT; 436 AA.
 AC 0SM911;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE LOC496632 protein (Fragment).
 GN Name=LOC496632;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 NCBI_TaxID=8364;
 [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole body;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strusberg R.L., Feingold R.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Wuzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Goughman J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Whole body;
 RC Klein S., Gerhard D.S.;
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL; BC087750; AAH87750.1; -, mRNA.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR000295; Prot_inh_serpin.
 DR InterPro; IPR00215; Prot_inh_serpin.
 DR Pfam; PF00780; SERPIN.1.
 DR PRINTS; PRO0780; LRU SERPIN1.
 DR SMART; SM00093; SERPIN.1.
 DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
 DR Serpin.
 KM NON_TER
 FT SEQUENCE 436 AA; 49692 MW; 07EB4D2A7446A34B CRC64;
 SQ
 Query Match 39.5%; Score 841; DB 2; Length 436;
 Best Local Similarity 42.1%; Pred. No. 1.8e-51;
 Matches 157; Conservative 94; Mismatches 120; Indels 2; Gaps 1;
 QY 41 QMAAKELARONMDLGFLLKKAFAFYNPGRNIFLPSLSTAFSMLCIGAOSTLDEIKQ 100
 DB 62 ESMPCIKIAFYNAFSGSLVRQIAADHPTENIFSPSISTVPMMLSGARSNTLNGIIE 121
 QY 101 G--FNPKMKERKOLHEGFHYIHELTKTDKLKISGNTLPIDQRLQPKRELEDAKPY 158
 DB 122 GLKFNSELTEEBEHNKGFQHLHLMLNDPNSKVOINSNALFIDKDLQIOKFVEDSKQFY 181
 QY 159 SAETILNPFONLEMAQOINDFISQKTHKINLNLENIDPGVMLLANYIFPARMKHEF 218
 DB 182 EATITGTFDHFNTERTATQIINTVAKNKTKITDLSSVDEETILVLYNYPFGWEKHF 241
 QY 219 DPNVTKEBDFLEKNSSVKVPMFERSGIYGVYDCLKSCTLEIPYOKNITAFILDEG 278
 DB 242 EKEMTKQGI FHVDENTVTVPMHGRNGMYVAVPDEKLGCTVQIPYKGNMTALFILDEG 301
 QY 279 KLAHLEKGLQVDFSRKKTLSRRVVDVSVPLMTGTPLDKTSLSTYGSKI FEEHGL 338
 DB 302 KLAQVEBALEKAVVSKWKLFRKRFVHLTPKLSISATITDLVXELSKLGTVDFSDSDL 361
 QY 339 TKLIAPRSLKVGAVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLIYSEK 398
 DB 362 SGIVDVTPLKVSQAVHVLVTSIDBTGAAGVTVMELPRLRYNPPVLMITYEPT 421
 QY 399 IPSVLFGLKIVNP 411
 DB 422 LRANLFWGRVNP 434
 RESULT 10
 Q8JIA6 SPHFU
 ID Q8JIA6 SPHFU PRELIMINARY; PRT; 426 AA.
 AC Q8JIA6;
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Alpha-1-antitrypsin (Fragment).
 OS Sphenodon punctatus (Hatteria) (Tuatara).
 OC Sphenodontia; Sphenodontia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Sphenodontia; Sphenodontidae; Sphenodon.
 OC NCBI_TaxID=8508;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.

RA Metcalf V.J., Brennan S.O., George P.M., Chambers G.K.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the serpin family.
 DR EMBL; AF375974; AA046107.1; -, mRNA.
 DR HSSP; P01009; 182X.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR000215; Prot_inh_serpin.
 DR Pfam; PF00079; Serpin.1.
 DR SMART; SM00093; SERPIN.1.
 DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
 DR Serpin.
 KM NON_TER
 FT SEQUENCE 426 AA; 48318 MW; 6D75C8737FE70950 CRC64;
 SQ
 Query Match 38.8%; Score 827; DB 2; Length 426;
 Best Local Similarity 39.6%; Pred. No. 1.7e-50;
 Matches 170; Conservative 93; Mismatches 142; Indels 24; Gaps 6;
 QY 1 MNPTGLAIFLAVALTVKGLLKPSFSPR-----NYKALSEVQGM---KQMAAKEL 48
 DB 1 MPTTILCLILAMFCF-----AYSHHPDHQHDHDKQKQTHAGAPPSKMTCHKI 54
 QY 49 ARQNDLGFLLKKAFAFYNPGRNIFLPSLSTAFSMLCIGAOSTLDEIKQ--FNPK 106
 DB 55 APSNADPAFPFYQIAAEADAKVFFSPVSI STAFAMLTGAKSTQSQIYEGIAFWLLE 114
 QY 107 MPEDLHEGFHYIHELTKTDKLKISGNTLPIDQRLQPKRELEDAKPYSAETILTN 166
 DB 115 IEBDEIHGHRHFWMSLSLDRILNMGALFIDKELKPIKPLDIXSFYASEGSSN 174
 QY 167 FQNLMAQOINDFISQKTHKINLNLENIDPGVMLLANYIFPARMKHEFDPNVKEE 226
 DB 175 FTSABAEKQINDIYKKTGELVDLVKNGCPDTMWLVYILKAWHPFNATREE 234
 QY 227 DFLKKNSSVKVPMFERSGIYGVYDCLKSCTT--LEIPYOKNITAFILDESKHLE 284
 DB 235 DFFVDGTSYKVVMMNDPSYNSLHDKKLSCLVQWVDLPQRAVVAATFILPDEKMQVE 294
 QY 285 KGIQVDFSRKKTLS--SRVVDVSVPLMTGTPLDKTSLSTYGSKI FEEHGLTKIA 342
 DB 295 DALSEVLTLEKSLRKRERIRHLSIPRFSISGYDVKELFRRMGVTEVFTNQADLSGIT 354
 QY 343 PHSRLKVGAVHKAELKMDERGTEGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSV 402
 DB 355 GSEELKVSRAVHKAELHENGTEBASTTYIELVPSLPPVVKLNRPFSLYDKTASV 414
 QY 403 LFLGKIVNP 411
 DB 415 LFWGKIVNP 423
 RESULT 11
 ID ALAT CERAB STANDARD; PRT; 396 AA.
 AC 000354;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
 DE antiprotease) (Fragment).
 GN Name=SERPIN1;
 OS Cercopithecus aethiops (Green monkey) (Griivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 OC Cercopithecoidea; Cercopithecinae; Cercopithecus.
 OC NCBI_TaxID=9534;
 RX [1]
 RP NUCLEOTIDE SEQUENCE [mRNA].
 RC TISSUE=Kidney;
 RA Yoshida K., Suzuki Y., Yamamoto K., Watanabe M., Shinohara H.;
 RT Cloning and sequencing of complementary DNAs encoding alpha-2-HS
 RT glycoprotein, alpha-1-antitrypsin, and beta-actin from african green
 RT monkey, Cercopithecus aethiops.;

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Inhibitor of serine proteases. Its primary target is
 CC elastase, but it also has a moderate affinity for plasmin and
 CC thrombin (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- DOMAIN: The reactive center loop (RCL) extends out from the body
 CC of the protein and directs binding to the target protease. The
 CC protease cleaves the serpin at the reactive site within the RCL,
 CC establishing a covalent linkage between the carboxyl group of the
 CC serpin reactive site and the serine hydroxyl of the protease. The
 CC resulting inactive serpin-protease complex is highly stable (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the serpin family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: AB004044; BAA20264.1; -; mRNA.
 CC HSSP: P01009; 1EZX.
 CC SMR: O00394; 25-386.
 CC GO: 0004867; F:serine-type endopeptidase inhibitor activity; NAS.
 CC GO: 0030162; P:regulation of proteolysis and peptidolysis; NAS.
 CC InterPro: IPR000215; Prot_inh_serpin.
 CC PANTHER: PTHR11461; Prot_inh_serpin; 1.
 CC Pfam: PF00079; Serpin; 1.
 CC SMART: SM00093; SERPIN; 1.
 CC PROSITE: PS00284; SERPIN; 1.
 CC KW Acute phase; Glycoprotein; Protease inhibitor;
 CC Serine protease inhibitor; Serpin; Signal.
 CC FT SIGNAL <1 2
 CC FT CHAIN 3 396
 CC FT REGION 351 370
 CC FT SITE 360 361
 CC FT CARBOHYD 48 48
 CC FT CARBOHYD 85 85
 CC FT CARBOHYD 123 123
 CC FT CARBOHYD 249 249
 CC FT NON_TER 1 1
 CC FT SEQUENCE 396 AA; 44587 MW; 1042EABFA0A2825 CRC64;
 SQ
 Query Match 37.2%; Score 792; DB 1; Length 396;
 Best Local Similarity 42.1%; Pred. No. 4,8e-48;
 Matches 153; Conservative 81; Mismatches 127; Indels 2; Gaps 1;

Db 394 TOK 396
 RESULT 12
 ID ALAT_PONPY STANDARD; PRT; 418 AA.
 AC OSRCW5; Q5NVR9; OSRF76;
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
 DE antitrypsinase).
 GN Name=SERPIN1;
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
 RC TISSUE=Heart, Kidney and Liver;
 RG The German cDNA consortium;
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Inhibitor of serine proteases. Its primary target is
 CC elastase, but it also has a moderate affinity for plasmin and
 CC thrombin (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- DOMAIN: The reactive center loop (RCL) extends out from the body
 CC of the protein and directs binding to the target protease. The
 CC protease cleaves the serpin at the reactive site within the RCL,
 CC establishing a covalent linkage between the carboxyl group of the
 CC serpin reactive site and the serine hydroxyl of the protease. The
 CC resulting inactive serpin-protease complex is highly stable (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the serpin family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: CR857285; CAH89581.1; -; mRNA.
 CC EMBL: CR858153; CAH90392.1; -; mRNA.
 CC EMBL: CR925936; CA129594.1; -; mRNA.
 CC SMR: OSRCW5; 47-418.
 CC InterPro: IPR000215; Prot_inh_serpin.
 CC PANTHER: PTHR11461; Prot_inh_serpin; 1.
 CC Pfam: PF00079; Serpin; 1.
 CC SMART: SM00093; SERPIN; 1.
 CC PROSITE: PS00284; SERPIN; 1.
 CC KW Acute phase; Glycoprotein; Protease inhibitor;
 CC Serine protease inhibitor; Serpin; Signal.
 CC FT SIGNAL 1 24
 CC FT CHAIN 25 418
 CC FT REGION 373 392
 CC FT SITE 382 383
 CC FT CARBOHYD 70 70
 CC FT CARBOHYD 107 107
 CC FT CARBOHYD 271 271
 CC FT CARBOHYD 289 289
 CC FT CONFLICT 289 289
 CC FT CONFLICT 305 305
 CC FT CONFLICT 332 332
 CC FT CONFLICT 336 404
 CC FT SEQUENCE 418 AA; 46861 MW; BF93D2080AEDE56 CRC64;
 SQ
 Query Match 37.1%; Score 790; DB 1; Length 418;
 Best Local Similarity 42.7%; Pred. No. 7,2e-48;
 Matches 155; Conservative 76; Mismatches 130; Indels 2; Gaps 1;

DR EMBL; D17725; BAA04579.1; -; mRNA.
 DR PIR; S54981; S54981.
 DR HSSP; P01009; 1QMB.
 DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
 DR InterPro; IPR000215; Prot_inh_serpin.
 DR Pfam; PF00079; Serpin; 1.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 DR Serpin; Signal.
 KW Serpin; Signal.
 FT SIGNAL 1 23 Potential.
 FT CHAIN 24 413 alpha-1-antiprotease E.
 SQ SEQUENCE 413 AA; 45684 MW; C0B86D6091639E2 CRC64;
 Query Match 36.9%; Score 785.5; DB 2; Length 413;
 Best Local Similarity 37.5%; Pred. No. 1.5e-47;
 Matches 155; Conservative 98; Mismatches 155; Indels 5; Gaps 2;

QY 1 NNPTGLAIFLAVLLTVKGLKPSFSPRYKALSEVQWKQMAKELARQNMDLGPKLL 60
 DB 1 MPPSVSRAL---LLLAGLGCLLPFLADAEQETAVSHEDHPACHRIAPSLAEFALSILY 57
 QY 61 KKLAFYNGRNIFLSPLSISTAFSMLCIAQDSTLDEIKQG--FNFRKMPKXDLHGPHY 118
 DB 58 KEVAHESNTNTTFPSFVSIALAPAMSLGAKGDTHTQVLEGLKFNLTETRAQIHGDFPH 117
 QY 119 IIEHLTKTQDLKLSIGNTFLIDRLQPKRKELEDAKNFYSAETILTNPQNLMAQKQIN 178
 DB 118 LHTVVRPSELQLAGNMLVHVENIKLQHKFLEDAKNLYGSAFLVDFRDPQATKIN 177
 QY 179 DFIQKTHGKINNLIINIDPQTMLLANTYFFPARKHEPDVNTYGEQDFLEKSSVXY 238
 DB 178 SHYKCKTRKIKVDLVQELARLIALVNVYFFPKGKEKPEPENTBEQPHVDATTVAV 237
 QY 239 PMWFRSGIYOVGDDKLSCTLEIPYQKNTAFILIPDESKLGHKGLQVDFSRWKTLL 298
 DB 238 PMMSRLGMYVMHRCSTLASTVLMNDYKGNATFLIPDESKQHLDTLTTELIAFGLAK 297
 QY 299 LSRRAVDVSPRLMHTGTDPLDKKTLSTYIGVSKIFEEHGLDTKLPARSLKGEAVHKAEL 358
 DB 298 SGLRSVTVPFKLSTISGTYDKLKLKLGITGVFSNNAADLSGTTEQBPPLKVSALHKAVL 357
 QY 359 KNDERGTGGAAGTGAQTLPMETPLVVKIDPKYLLIYSEKIPSVLFLGKIIVP 411
 DB 358 TIDERGTGAAGASFVELIPESVDSITLDRPFLVIYSHKISPLFVGKVDVP 410

RESULT 15
 ALAT_RAT STANDARD; PRT; 411 AA.
 ID ALAT_RAT
 AC P17475; O6AYZ5;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Alpha-1-antiprotease precursor (Alpha-1-antitrypsin) (Alpha-1-proteinase inhibitor).
 GN Name=Serpin1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath; Muridae; Muridae; Murinae; Rattus.
 OC NCBI_TaxId=10116;
 GN NCBI_TaxId=10116;
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC STRAIN=Miscari; TISSUE=Liver;
 RX MEDLINE=91035351; PubMed=2229024;
 RA Mitsumori Y., Sonda M., Ohkubo K., Takami N., Oda K., Ikehara Y.;
 RT "Molecular cloning and sequencing of the cDNA of rat alpha 1-protease inhibitor and its expression in COS-1 cells";
 RL J. Biochem. 108:230-234 (1990).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Testis;
 RG NIH - Mammalian Gene Collection (MGC) project;

RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE [MRNA] OF 4-411, PROTEIN SEQUENCE OF 25-57, AND
 RP TISSUE SPECIFICITY.
 RC TISSUE=Liver;
 RX MEDLINE=90148955; PubMed=2302382;
 RA Chao S., Chai K.X., Chao L., Chao J.;
 RT "Molecular cloning and primary structure of rat alpha 1-antitrypsin";
 RL Biochemistry 29:323-329 (1990).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [MRNA] OF 188-389.
 RC TISSUE=Liver;
 RA Fink I.L., Bailey T., Morkin E.;
 RL Submitted (Aug-1989) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Inhibitor of serine proteases. The primary target is elastase, but also has a moderate affinity for plasmin and thrombin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- DOMAIN: The reactive center loop (RCL) extends out from the body of the protein and directs binding to the target protease. The protease cleaves the serpin at the reactive site within the RCL, establishing a covalent linkage between the carboxyl group of the serpin reactive site and the serine hydroxyl of the protease. The resulting inactive serpin-protease complex is highly stable (By similarity).
 CC -1- SIMILARITY: Belongs to the serpin family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - CC use as long as its content is in no way modified and this statement is not removed.
 CC EMBL; D00675; BAA00579.1; -; mRNA.
 CC EMBL; BC078824; AAH78824.1; -; mRNA.
 CC EMBL; M32247; AAA40788.1; -; mRNA.
 CC EMBL; X16273; CAA34349.1; -; mRNA.
 CC PIR; A33892; ITRT.
 CC HSSP; P01009; 1QMB.
 CC SMR; P17475; 39-411.
 CC DR Ensembl; ENSRNOC0000032669; Rattus norvegicus.
 CC DR InterPro; IPR000215; Prot_inh_serpin.
 CC DR PANTHER; PTHR11461; Prot_inh_serpin; 1.
 CC DR Pfam; PF00079; Serpin; 1.
 CC DR SMART; SM00093; SERPIN; 1.
 CC DR PROSITE; PS00284; SERPIN; 1.
 CC KW Acute phase; Direct protein sequencing; Glycoprotein;
 CC KW Protease inhibitor; Serine protease inhibitor; Serpin; Signal.
 CC FT SIGNAL 1 24
 CC FT CHAIN 25 411 Alpha-1-antiprotease.
 CC FT REGION 367 386 RCL.
 CC FT SITE 376 377 Reactive bond.
 CC FT CARBOHYD 64 64 N-linked (GlcNAc...) (potential).
 CC FT CARBOHYD 101 101 N-linked (GlcNAc...) (potential).
 CC FT CARBOHYD 265 265 N-linked (GlcNAc...) (potential).
 CC FT CONFLICT 14 14 A -> G (in Ref. 1).
 CC FT CONFLICT 84 84 L -> V (in Ref. 1 and 2; AAH78824).
 CC FT CONFLICT 247 247 M -> I (in Ref. 4).
 CC FT CONFLICT 248 248 H -> Y (in Ref. 1).
 CC FT CONFLICT 318 318 K -> N (in Ref. 1).
 CC FT CONFLICT 322 322 S -> D (in Ref. 4).
 SQ SEQUENCE 411 AA; 46136 MW; B4245CFE21C5C761 CRC64;
 Query Match 36.9%; Score 785; DB 1; Length 411;
 Best Local Similarity 38.8%; Pred. No. 1.6e-47;
 Matches 161; Conservative 94; Mismatches 150; Indels 10; Gaps 5;

QY 1 NNPTGLAIFLAVLLTVKGLKPSFSPRYKALSEVQWKQMAKELARQNMDLGPKLL 60
 DB 1 MAPSISRGILLIALALC---CLAPSLADAGE--TTSQDDGSPYTRKISSNADAFSLY 56
 QY 61 KKLAFYNGRNIFLSPLSISTAFSMLCIAQDSTLDEIKQG--FNFRKMPKXDLHGPHY 118

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Db      57 RELVHQSNTSNIFFSFMSITTAFAFWLSTGSKGDTFRKQILEGLEBNLTQIPEADITHKAFHH 116
Qy      119 IHHELTQKTODLKLSIGNTLFIDQLOPQKFTLEDKRFYSAETILITVFONLEMAQOIN 178
Db      117 LLQTLNRPDSSELQNLNTGGLFVNKNLKLVERKPLEEVKNYHSEAFSVNPADEBEAKVYN 176
Qy      179 DPLSOKTHGKINLLENIDPGVMLANYIFPRARWKHEFPDENVTKBEDPFLKNSSVKV 238
Db      177 DYVEKGTOGKIVDLMKQLEBDTVFALVNYIFPKGKWKRPFNPERTRDADFVHDKSITVKV 236
Qy      239 PPMFRSGIYOVGYDDKLSCTILLEIPYOKNITAFILPDDEGKLKHEKGLQVDTFSRWKTL 298
Db      237 PPMNRRLGMPDMHYCSTLSSWVLMMDYLGNAATAFILPDGKQOHLEQTLTKDLISRF--L 294
Qy      299 LSR--RVVDVSVPLHMTGTFDLKKTLSYIGVSKIPEHGDLTKIAPHRSLKGBAYHKA 356
Db      295 LNRQTRSAILFFPLDSISGTYNLKTLSSLSGLITRVFNNDADLSGITBEDAPKLQAVHKA 354
Qy      357 ELKMDERGTGAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSPVLPFGKI VNP 411
Db      355 VLTI DERGTGAAGTVAVPMSLPPOVKPDHPRFI PMIVESRQSPLFVGKVIDP 409

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Search completed: March 31, 2006, 09:50:05
 Job time : 235 secs

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OM protein - protein search, using sw model

Run on: March 31, 2006, 09:51:09 ; Search time 167 Seconds
(without alignment)
1035.816 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 2130
Sequence: 1 MNPTLGAIPLAVLITVKG.....YSEKIPSEVLGKIVNPICK 414

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2130	100.0	414	3	US-09-755-665-14 Sequence 14, App1
2	2130	100.0	414	3	US-09-755-665-55 Sequence 55, App1
3	2130	100.0	414	3	US-09-755-665-56 Sequence 56, App1
4	2130	100.0	414	4	US-10-168-425-12 Sequence 12, App1
5	2130	100.0	414	4	US-10-629-248-14 Sequence 14, App1
6	2130	100.0	414	4	US-10-629-248-55 Sequence 55, App1
7	2130	100.0	414	4	US-10-629-248-56 Sequence 56, App1
8	2130	100.0	415	4	US-10-012-542-134 Sequence 134, App
9	2130	100.0	415	4	US-10-115-123-134 Sequence 134, App
10	2130	100.0	415	4	US-10-800-834-134 Sequence 134, App
11	2114	99.2	431	4	US-10-276-774-2202 Sequence 2202, Ap
12	1798	84.4	361	3	US-09-755-665-57 Sequence 57, App1
13	1798	84.4	361	4	US-10-629-248-57 Sequence 57, App1
14	842	39.5	377	4	US-10-037-417-66 Sequence 67, App1
15	840	39.4	371	4	US-10-023-634-87 Sequence 87, App1
16	837	39.3	377	3	US-09-823-187-31 Sequence 31, App1
17	786	36.9	418	5	US-10-741-600-1216 Sequence 1216, Ap
18	786	36.9	418	5	US-10-741-600-1217 Sequence 1217, Ap
19	786	36.9	418	5	US-10-741-600-1218 Sequence 1218, Ap
20	786	36.9	418	5	US-10-741-600-1219 Sequence 1219, Ap
21	786	36.9	418	5	US-10-741-600-1220 Sequence 1220, Ap
22	786	36.9	418	5	US-10-741-600-1221 Sequence 1221, Ap
23	786	36.9	418	5	US-10-741-600-1222 Sequence 1222, Ap
24	785	36.9	363	3	US-09-755-665-58 Sequence 58, App1
25	785	36.9	363	4	US-10-629-248-58 Sequence 58, App1
26	785	36.9	394	4	US-09-993-180-6 Sequence 6, App1
27	785	36.9	394	4	US-10-025-514-2 Sequence 2, App1

28	785	36.9	394	4	US-10-365-738-1 Sequence 1, App1
29	785	36.9	394	6	US-11-077-276-2 Sequence 2, App1
30	785	36.9	395	5	US-10-914-863-2 Sequence 2, App1
31	785	36.9	418	4	US-10-037-340-286 Sequence 286, App
32	785	36.9	418	4	US-10-411-037-22 Sequence 22, App1
33	785	36.9	418	4	US-10-411-026-22 Sequence 22, App1
34	785	36.9	418	4	US-10-410-962-22 Sequence 22, App1
35	785	36.9	418	4	US-10-411-049-22 Sequence 22, App1
36	785	36.9	418	4	US-10-408-765A-2304 Sequence 2304, Ap
37	785	36.9	418	4	US-10-410-930-22 Sequence 22, App1
38	785	36.9	418	4	US-10-410-997-22 Sequence 22, App1
39	785	36.9	418	4	US-10-411-012-22 Sequence 22, App1
40	785	36.9	418	4	US-10-287-994-22 Sequence 22, App1
41	785	36.9	418	4	US-10-410-913-22 Sequence 22, App1
42	785	36.9	418	5	US-10-410-980-22 Sequence 22, App1
43	785	36.9	418	5	US-10-971-461-15 Sequence 15, App1
44	785	36.9	418	5	US-10-410-897-22 Sequence 22, App1
45	785	36.9	418	5	US-10-492-261-22 Sequence 22, App1

ALIGNMENTS

RESULT 1
US-09-755-665-14 Application US/09755665
Sequence 14, App1
Patent No. US20020107186A1
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tallon, Bruce B.
APPLICANT: Spaderna, Steven K.
APPLICANT: Speyck, Kimberly A.
APPLICANT: MacDougall, John
TITLE OR INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-09-755-665-14
Query Match 100.0%; Score 2130; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNPTLGAIPLAVLITVKGILKPSFSPRYKALSEVGWQMAAKELARQNDLGFKL 60
DB 1 MNPTLGAIPLAVLITVKGILKPSFSPRYKALSEVGWQMAAKELARQNDLGFKL 60
QY 61 KKLAFNPGNITLSPISISTAFSMCLGQDSITLDEIKGFNRKPEKDLHGFRYIT 120
DB 61 KKLAFNPGNITLSPISISTAFSMCLGQDSITLDEIKGFNRKPEKDLHGFRYIT 120
QY 121 HELTQKTDKLSIGNTLFDQRLQPKFLDPAKFFSSETLITFQNLMAQKQNDP 180
DB 121 HELTQKTDKLSIGNTLFDQRLQPKFLDPAKFFSSETLITFQNLMAQKQNDP 180
QY 181 ISQTHGKINLLENIDPGTMLANVIFFRARWKIEPDNVTKEEDFLEKNSVYKPM 240
DB 181 ISQTHGKINLLENIDPGTMLANVIFFRARWKIEPDNVTKEEDFLEKNSVYKPM 240
QY 241 MFRSGIYGVGDYDKSCTTLEIPYQKNTAIFLLPDEGKLKHEKGLQVDTFSRWKTLIS 300
DB 241 MFRSGIYGVGDYDKSCTTLEIPYQKNTAIFLLPDEGKLKHEKGLQVDTFSRWKTLIS 300
QY 301 RRVVDVSVPLHMTGTFTDLKKTLSYGVSKIPEFHGDLTKIAPHRSLLKVGEAVHKAELKM 360

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Db      301 RRVADVSVPLHMTGTFDLKKTLSYIGVSKIPEEHGDLTIAPHRSLKVGAEVHKAELKM 360
Qy      361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKISPVLFGLKIVNPIGK 414
Db      361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKISPVLFGLKIVNPIGK 414

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RESULT 2

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US-09-755-665-55
; Sequence 55, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce E.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-55

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Query Match      100.0%; Score 2130; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MNPTGLAIFLAVLITVKGILKPSFSPRYKALSEVQWKQMAKELARQNMNDLGFKLL 60
Db      1 MNPTGLAIFLAVLITVKGILKPSFSPRYKALSEVQWKQMAKELARQNMNDLGFKLL 60
Qy      61 KKLAFNPGRNITFLSPISISTAFSMCLGADSTLDEIKQGFNFRMPKDLHEGFHYII 120
Db      61 KKLAFNPGRNITFLSPISISTAFSMCLGADSTLDEIKQGFNFRMPKDLHEGFHYII 120
Qy      121 HELTQKTQDLKLSIGNTLFIIDQRLQPKRFLDANKFYSAETILTNFQNLMAQKQINDF 180
Db      121 HELTQKTQDLKLSIGNTLFIIDQRLQPKRFLDANKFYSAETILTNFQNLMAQKQINDF 180
Qy      181 ISQKTHGKINNLIENIDPGTVMILANYIFFRARWKHEPDNVTKEEDFLEKNSVYKVM 240
Db      181 ISQKTHGKINNLIENIDPGTVMILANYIFFRARWKHEPDNVTKEEDFLEKNSVYKVM 240
Qy      241 MFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLIS 300
Db      241 MFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLIS 300
Qy      301 RRVADVSVPLHMTGTFDLKKTLSYIGVSKIPEEHGDLTIAPHRSLKVGAEVHKAELKM 360
Db      301 RRVADVSVPLHMTGTFDLKKTLSYIGVSKIPEEHGDLTIAPHRSLKVGAEVHKAELKM 360
Qy      361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKISPVLFGLKIVNPIGK 414
Db      361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKISPVLFGLKIVNPIGK 414

```

RESULT 3

```

US-09-755-665-56
; Sequence 56, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud

```

```

; APPLICANT: Tailon, Bruce E.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-56

```

```

Query Match      100.0%; Score 2130; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 MNPTGLAIFLAVLITVKGILKPSFSPRYKALSEVQWKQMAKELARQNMNDLGFKLL 60
Db      1 MNPTGLAIFLAVLITVKGILKPSFSPRYKALSEVQWKQMAKELARQNMNDLGFKLL 60
Qy      61 KKLAFNPGRNITFLSPISISTAFSMCLGADSTLDEIKQGFNFRMPKDLHEGFHYII 120
Db      61 KKLAFNPGRNITFLSPISISTAFSMCLGADSTLDEIKQGFNFRMPKDLHEGFHYII 120
Qy      121 HELTQKTQDLKLSIGNTLFIIDQRLQPKRFLDANKFYSAETILTNFQNLMAQKQINDF 180
Db      121 HELTQKTQDLKLSIGNTLFIIDQRLQPKRFLDANKFYSAETILTNFQNLMAQKQINDF 180
Qy      181 ISQKTHGKINNLIENIDPGTVMILANYIFFRARWKHEPDNVTKEEDFLEKNSVYKVM 240
Db      181 ISQKTHGKINNLIENIDPGTVMILANYIFFRARWKHEPDNVTKEEDFLEKNSVYKVM 240
Qy      241 MFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLIS 300
Db      241 MFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLIS 300
Qy      301 RRVADVSVPLHMTGTFDLKKTLSYIGVSKIPEEHGDLTIAPHRSLKVGAEVHKAELKM 360
Db      301 RRVADVSVPLHMTGTFDLKKTLSYIGVSKIPEEHGDLTIAPHRSLKVGAEVHKAELKM 360
Qy      361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKISPVLFGLKIVNPIGK 414
Db      361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKISPVLFGLKIVNPIGK 414

```

RESULT 4

```

US-10-168-425-12
; Sequence 12, Application US/10168425
; Publication No. US20030124706A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YANG, Junming
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: BURFORD, Neil
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LU, Dying Aina M.
; APPLICANT: REDDY, Roopa
; APPLICANT: YUE, Henry
; APPLICANT: NGUYEN, Daniel B.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YAO, Monique G.
; APPLICANT: LAU, Preeti
; TITLE OF INVENTION: PROTEASES
; FILE REFERENCE: PI-0003 PCT
; CURRENT APPLICATION NUMBER: US/10/168,425
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/172,055; 60/177,334; 60/178,884; 60/179,903

```

PRIOR FILING DATE: 1999-12-23; 2000-01-21; 2000-01-28; 2000-02-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PERL Program
SEQ ID NO: 12
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030124706A1 7257324CD1
US-10-168-425-12

Query Match 100.0%; Score 2130; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVLLTVKGLKPSFPRNTKALSEVQGWKQMAAKELARQNDLGFYII 60
DB 1 MNPTGLAIFLAVLLTVKGLKPSFPRNTKALSEVQGWKQMAAKELARQNDLGFYII 60
QY 61 KCLAFYNGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
DB 61 KCLAFYNGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
QY 121 HELTQKQDCLKSIGNTLFIIDQRLQPKRFLKEDAKNFYSATLITNQNLEMAQKQINDF 180
DB 121 HELTQKQDCLKSIGNTLFIIDQRLQPKRFLKEDAKNFYSATLITNQNLEMAQKQINDF 180
QY 181 ISQKTHGKINNLINIDPGTVMLANIIFPRARKHEDPDVNTKEDPFLKNSSVKVP 240
DB 181 ISQKTHGKINNLINIDPGTVMLANIIFPRARKHEDPDVNTKEDPFLKNSSVKVP 240
QY 241 MPRSGIYQVGYDDKSCITLIEIPYQKNITAFILPDGSKLKHLEKGQVDTFSRWKTLIS 300
DB 241 MPRSGIYQVGYDDKSCITLIEIPYQKNITAFILPDGSKLKHLEKGQVDTFSRWKTLIS 300
QY 301 RRVVDVSVPRLHMTGTFDLKKTLSYIGSVSKIPEHGDLTAKAPRSLKVGSAVHAKELKM 360
DB 301 RRVVDVSVPRLHMTGTFDLKKTLSYIGSVSKIPEHGDLTAKAPRSLKVGSAVHAKELKM 360
QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSKIDSVLFLGKIIVPIGK 414
DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSKIDSVLFLGKIIVPIGK 414

RESULT 5

US-10-629-248-14
Sequence 14, Application US/10629248
Publication No. US2004011671A1
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tallon, Bruce E.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/10/629, 248
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/755, 665
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174, 724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-10-629-248-14

Query Match 100.0%; Score 2130; DB 4; Length 414;

Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVLLTVKGLKPSFPRNTKALSEVQGWKQMAAKELARQNDLGFYII 60
DB 1 MNPTGLAIFLAVLLTVKGLKPSFPRNTKALSEVQGWKQMAAKELARQNDLGFYII 60
QY 61 KCLAFYNGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
DB 61 KCLAFYNGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
QY 121 HELTQKQDCLKSIGNTLFIIDQRLQPKRFLKEDAKNFYSATLITNQNLEMAQKQINDF 180
DB 121 HELTQKQDCLKSIGNTLFIIDQRLQPKRFLKEDAKNFYSATLITNQNLEMAQKQINDF 180
QY 181 ISQKTHGKINNLINIDPGTVMLANIIFPRARKHEDPDVNTKEDPFLKNSSVKVP 240
DB 181 ISQKTHGKINNLINIDPGTVMLANIIFPRARKHEDPDVNTKEDPFLKNSSVKVP 240
QY 241 MPRSGIYQVGYDDKSCITLIEIPYQKNITAFILPDGSKLKHLEKGQVDTFSRWKTLIS 300
DB 241 MPRSGIYQVGYDDKSCITLIEIPYQKNITAFILPDGSKLKHLEKGQVDTFSRWKTLIS 300
QY 301 RRVVDVSVPRLHMTGTFDLKKTLSYIGSVSKIPEHGDLTAKAPRSLKVGSAVHAKELKM 360
DB 301 RRVVDVSVPRLHMTGTFDLKKTLSYIGSVSKIPEHGDLTAKAPRSLKVGSAVHAKELKM 360
QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSKIDSVLFLGKIIVPIGK 414
DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSKIDSVLFLGKIIVPIGK 414

RESULT 6

US-10-629-248-55
Sequence 55, Application US/10629248
Publication No. US2004011671A1
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tallon, Bruce E.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/10/629, 248
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/755, 665
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174, 724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 55
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-10-629-248-55

Query Match 100.0%; Score 2130; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 1.1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVLLTVKGLKPSFPRNTKALSEVQGWKQMAAKELARQNDLGFYII 60
DB 1 MNPTGLAIFLAVLLTVKGLKPSFPRNTKALSEVQGWKQMAAKELARQNDLGFYII 60
QY 61 KCLAFYNGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
DB 61 KCLAFYNGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
QY 121 HELTQKQDCLKSIGNTLFIIDQRLQPKRFLKEDAKNFYSATLITNQNLEMAQKQINDF 180
DB 121 HELTQKQDCLKSIGNTLFIIDQRLQPKRFLKEDAKNFYSATLITNQNLEMAQKQINDF 180

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Db 121 HELTQKTODLKLKISGNTLFIIDRLQPKFLEDAKNFYSAETILTNFONLEMAQKQINDF 180
Qy 181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRAMKHEFDPNVTKEEDFLEKNSSVKVP 240
Db 181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRAMKHEFDPNVTKEEDFLEKNSSVKVP 240
Qy 241 MFRSGIYQVGYDDKLSCTTLEIPYQKNITAFILPDEGKLEKGLQVDTFSRMKTTLS 300
Db 241 MFRSGIYQVGYDDKLSCTTLEIPYQKNITAFILPDEGKLEKGLQVDTFSRMKTTLS 300
Qy 301 RRVDVSVRLHMTGTGTFDLKKTLSYIGVSKIFEEHDLTKIAPHRSKLVGEAVHKAELKM 360
Db 301 RRVDVSVRLHMTGTGTFDLKKTLSYIGVSKIFEEHDLTKIAPHRSKLVGEAVHKAELKM 360
Qy 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYNPIGK 414
Db 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYNPIGK 414

RESULT 7
US-10-629-248-56
; Sequence 56, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tallon, Bruce B.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/10/629,248
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/755,665
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 56
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-629-248-56

Query Match 100.0%; Score 2130; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 1,1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPITGLAIFLAVLLTVGKLKPSFSPRYKALSEVOGKQMAKELARQNMDDGFKLL 60
Db 1 MNPITGLAIFLAVLLTVGKLKPSFSPRYKALSEVOGKQMAKELARQNMDDGFKLL 60
Qy 61 KCLAFNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKOGFNFRKMPKEDLHEGFHYII 120
Db 61 KCLAFNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKOGFNFRKMPKEDLHEGFHYII 120
Qy 121 HELTQKTODLKLKISGNTLFIIDRLQPKFLEDAKNFYSAETILTNFONLEMAQKQINDF 180
Db 121 HELTQKTODLKLKISGNTLFIIDRLQPKFLEDAKNFYSAETILTNFONLEMAQKQINDF 180
Qy 181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRAMKHEFDPNVTKEEDFLEKNSSVKVP 240
Db 181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRAMKHEFDPNVTKEEDFLEKNSSVKVP 240
Qy 241 MFRSGIYQVGYDDKLSCTTLEIPYQKNITAFILPDEGKLEKGLQVDTFSRMKTTLS 300
Db 241 MFRSGIYQVGYDDKLSCTTLEIPYQKNITAFILPDEGKLEKGLQVDTFSRMKTTLS 300
Qy 301 RRVDVSVRLHMTGTGTFDLKKTLSYIGVSKIFEEHDLTKIAPHRSKLVGEAVHKAELKM 360
Db 301 RRVDVSVRLHMTGTGTFDLKKTLSYIGVSKIFEEHDLTKIAPHRSKLVGEAVHKAELKM 360
Qy 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYNPIGK 414
Db 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYNPIGK 414
```

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Qy 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYNPIGK 414
Db 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYNPIGK 414

RESULT 8
US-10-012-542-134
; Sequence 134, Application US/10012542
; Publication No. US20030044851A1
; GENERAL INFORMATION:
; APPLICANT: Ruden et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino
; OTHER INFORMATION: acids
US-10-012-542-134

Query Match 100.0%; Score 2130; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 1,1e-178;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPITGLAIFLAVLLTVGKLKPSFSPRYKALSEVOGKQMAKELARQNMDDGFKLL 60
Db 1 MNPITGLAIFLAVLLTVGKLKPSFSPRYKALSEVOGKQMAKELARQNMDDGFKLL 60
Qy 61 KCLAFNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKOGFNFRKMPKEDLHEGFHYII 120
Db 61 KCLAFNPGRNIFLSPLSISTAFSMLCLGAQDSTLDEIKOGFNFRKMPKEDLHEGFHYII 120
Qy 121 HELTQKTODLKLKISGNTLFIIDRLQPKFLEDAKNFYSAETILTNFONLEMAQKQINDF 180
Db 121 HELTQKTODLKLKISGNTLFIIDRLQPKFLEDAKNFYSAETILTNFONLEMAQKQINDF 180
Qy 181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRAMKHEFDPNVTKEEDFLEKNSSVKVP 240
Db 181 ISQKTHGKINNLIENIDPGTVMLLANYIFPRAMKHEFDPNVTKEEDFLEKNSSVKVP 240
Qy 241 MFRSGIYQVGYDDKLSCTTLEIPYQKNITAFILPDEGKLEKGLQVDTFSRMKTTLS 300
Db 241 MFRSGIYQVGYDDKLSCTTLEIPYQKNITAFILPDEGKLEKGLQVDTFSRMKTTLS 300
Qy 301 RRVDVSVRLHMTGTGTFDLKKTLSYIGVSKIFEEHDLTKIAPHRSKLVGEAVHKAELKM 360
Db 301 RRVDVSVRLHMTGTGTFDLKKTLSYIGVSKIFEEHDLTKIAPHRSKLVGEAVHKAELKM 360
Qy 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYNPIGK 414
Db 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLLIYSEKIPSVLFLGKIYNPIGK 414
```


Db 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFGKIYVPIGK 414

RESULT 9

US-10-115-123-134
Sequence 134, Application US/10115123
Publication No. US2003006515A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P2029G30AP1D2
CURRENT APPLICATION NUMBER: US/10/115,123
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: PCT/US99/13418
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/089,507
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,508
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,509
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,510
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/090,112
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090,113
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 134
LENGTH: 415
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (415)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-115-123-134

Query Match 100.0%; Score 2130; DB 4; Length 415;

Best Local Similarity 100.0%; Pred. No. 1.1e-178;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTLGALFLAVLLTVYGLLKPSFSPRYKALSEVQGMKORMAAKELARONMDLGFKLL 60
DB 1 MNPTLGALFLAVLLTVYGLLKPSFSPRYKALSEVQGMKORMAAKELARONMDLGFKLL 60
QY 61 KKLAFYVPGNIFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
DB 61 KKLAFYVPGNIFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
QY 121 HELTQTKODKLSIGNTLFLDQRLQPKRFLBDKAKFYSAETLLTNFQNLMAQKQINDF 180
DB 121 HELTQTKODKLSIGNTLFLDQRLQPKRFLBDKAKFYSAETLLTNFQNLMAQKQINDF 180
QY 181 ISQKTKGKINNLENIIDPGVTMLANYIFPRARKKHEFDNVTKEEDFLEKSSVYVPM 240
DB 181 ISQKTKGKINNLENIIDPGVTMLANYIFPRARKKHEFDNVTKEEDFLEKSSVYVPM 240
QY 241 MFRSGIYQVGYDDKLSCTTLEIPIYQKNITAIIFLPDEGKLNLEKGLQVDTFSRWKTLIS 300
DB 241 MFRSGIYQVGYDDKLSCTTLEIPIYQKNITAIIFLPDEGKLNLEKGLQVDTFSRWKTLIS 300
QY 301 RRVVDVSVPLRMTGTFPDLLKKTLSYGVSKIFEEHGLTKIAPRSLKVGSAVHKAELKM 360
DB 301 RRVVDVSVPLRMTGTFPDLLKKTLSYGVSKIFEEHGLTKIAPRSLKVGSAVHKAELKM 360
QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFGKIYVPIGK 414
DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFGKIYVPIGK 414

RESULT 10

US-10-800-834-134

Sequence 134, Application US/10800834
Publication No. US20040146930A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: P2029P1D3
CURRENT APPLICATION NUMBER: US/10/800,834
CURRENT FILING DATE: 2004-03-16
PRIOR APPLICATION NUMBER: 10/115,123
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 09/461,325
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: PCT/US99/13418
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 60/089,507
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,508
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,509
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089,510
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/090,112
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090,113
PRIOR FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 134
LENGTH: 415
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (415)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-800-834-134

Query Match 100.0%; Score 2130; DB 4; Length 415;

Best Local Similarity 100.0%; Pred. No. 1.1e-178;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTLGALFLAVLLTVYGLLKPSFSPRYKALSEVQGMKORMAAKELARONMDLGFKLL 60
DB 1 MNPTLGALFLAVLLTVYGLLKPSFSPRYKALSEVQGMKORMAAKELARONMDLGFKLL 60
QY 61 KKLAFYVPGNIFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
DB 61 KKLAFYVPGNIFLSPSISTAFSMLCLGAQDSTLDEIKQGFNRKMPKEDLHGFYII 120
QY 121 HELTQTKODKLSIGNTLFLDQRLQPKRFLBDKAKFYSAETLLTNFQNLMAQKQINDF 180
DB 121 HELTQTKODKLSIGNTLFLDQRLQPKRFLBDKAKFYSAETLLTNFQNLMAQKQINDF 180
QY 181 ISQKTKGKINNLENIIDPGVTMLANYIFPRARKKHEFDNVTKEEDFLEKSSVYVPM 240
DB 181 ISQKTKGKINNLENIIDPGVTMLANYIFPRARKKHEFDNVTKEEDFLEKSSVYVPM 240
QY 241 MFRSGIYQVGYDDKLSCTTLEIPIYQKNITAIIFLPDEGKLNLEKGLQVDTFSRWKTLIS 300
DB 241 MFRSGIYQVGYDDKLSCTTLEIPIYQKNITAIIFLPDEGKLNLEKGLQVDTFSRWKTLIS 300
QY 301 RRVVDVSVPLRMTGTFPDLLKKTLSYGVSKIFEEHGLTKIAPRSLKVGSAVHKAELKM 360
DB 301 RRVVDVSVPLRMTGTFPDLLKKTLSYGVSKIFEEHGLTKIAPRSLKVGSAVHKAELKM 360
QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFGKIYVPIGK 414
DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFGKIYVPIGK 414

RESULT 11

```
US-10-276-774-2202
; Sequence 2202, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245a1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; PRIOR FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2202
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2202
```

Query Match 99.2%; Score 2114; DB 4; Length 431;

Best Local Similarity 99.3%; Pred. No. 2.9e-177;

Matches 411; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 MNFTGLAIFLAVLITVKGILKPSFSPRNKALSEVQGMKQMAKELARQNMDELGFKL 60
DB 18 MNFTGLAIFLAVLITVKGILKPSFSPRNKALSEVQGMKQMAKELARQNMDELGFKL 77
QY 61 KKLAFNPGRNITLSPISISTAFSMLCLGAQDSTLDEIKQGFNRRKPEKDLHEGFYII 120
DB 78 KKLAFNPGRNITLSPISISTAFSMLCLGAQDSTLDEIKQGFNRRKPEKDLHEGFYII 137
QY 121 HELTOKTODKLSIGNTLFIIDORLOPORKELEDANKFYSAEITLTNPNLEMAKQINDP 180
DB 138 HELTOKTODKLSIGNTLFIIDORLOPORKELEDANKFYSAEITLTNPNLEMAKQINDP 197
QY 181 ISQTHGKINNLINIDPQTVMLLANYIFPRARKHGFDPNVTKEEDFLEKSSVYKVP 240
DB 198 ISQTHGKINNLINIDPQTVMLLANYIFPRARKHGFDPNVTKEEDFLEKSSVYKVP 257
QY 241 MFRSGIYQVGYDDKLSCTTLEIPIYQKNITAIIFLPDEGKIKHLEKGLQVDTFSRMTLLS 300
DB 258 MFRSGIYQVGYDDKLSCTTLEIPIYQKNITAIIFLPDEGKIKHLEKGLQVDTFSRMTLLS 317
QY 301 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSILKGEAVHKAELK 360
DB 318 RRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSILKGEAVHKAELK 377
QY 361 DERGTGAAGTAGTLPMTPLVVKIDKPYLLIYSEKIPSVLPFGKIIVPIGK 414
DB 378 DERGTGAAGTAGTLPMTPLVVKIDKPYLLIYSEKIPSVLPFGKIIVPIGK 431
```

RESULT 12

```
US-09-755-665-57
; Sequence 57, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce E.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
```

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 57

LENGTH: 361

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: VARIANT

LOCATION: (1)..(361)

OTHER INFORMATION: wherein Xaa is any amino acid as defined in the

OTHER INFORMATION: specification

US-09-755-665-57

Query Match 84.4%; Score 1798; DB 3; Length 361;

Best Local Similarity 96.7%; Pred. No. 1.5e-149;

Matches 349; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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QY 54 DLGFKLLKLAFNPGRNITLSPISISTAFSMLCLGAQDSTLDEIKQGFNRRKPEKDLH 113
DB 1 DLGFKLLKLAFNPGRNITLSPISISTAFSMLCLGAQDSTLDEIKQGFNRRKPEKDLH 60
QY 114 EGFHYIHELTKTODKLSIGNTLFIIDORLOPORKELEDANKFYSAEITLTNPNLEMA 173
DB 61 EGFHYIHELTKTODKLSIGNTLFIIDORLOPORKELEDANKFYSAEITLTNPNLEMA 120
QY 174 QKQINDFISQTHGKINNLINIDPQTVMLLANYIFPRARKHGFDPNVTKEEDFLEKX 233
DB 121 QKQINDFISQTHGKINNLINIDPQTVMLLANYIFPRARKHGFDPNVTKEEDFLEKX 180
QY 234 SSYKVPMMFRSGIYQVGYDDKLSCTTLEIPIYQKNITAIIFLPDEGKIKHLEKGLQVDTFS 293
DB 181 SSYKVPMMFRSGIYQVGYDDKLSCTTLEIPIYQKNITAIIFLPDEGKIKHLEKGLQVDTFS 240
QY 294 RMTLLSRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSILKGEAV 353
DB 241 RMTLLSRVVDVSVPRLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSILKGEAV 300
QY 354 HKAELKMDERGTGAAGTAGTLPMTPLVVKIDKPYLLIYSEKIPSVLPFGKIIVPIG 413
DB 301 HKAELKMDERGTGAAGTAGTLPMTPLVVKIDKPYLLIYSEKIPSVLPFGKIIVPIG 360
QY 414 K 414
DB 361 K 361
```

RESULT 13

```
US-10-629-248-57
; Sequence 57, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce E.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/10/629,248
; PRIOR FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/755,665
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 57
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(361)
```

OTHER INFORMATION: wherein Xaa is any amino acid as defined in the
OTHER INFORMATION: specification
US-10-629-248-57

Query Match 84.4%; Score 1798; DB 4; Length 361;
Best Local Similarity 96.7%; Pred. No. 1,5e-145;
Matches 349; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 54 DLGFLKLKLAFLYNGRNIPLSPISITAFSMLCLGADOSTLDEIKOGFNPKMEKOLH 113
DB 1 DLGFLKLKLAFLYNGRNIPLSPISITAFSMLCLGADOSTLDEIKOGFNPKMEKOLH 60
QY 114 EGFYIIHETLQKTODLKLISGNTLFIQDLQPKFLEDAKNFYSAETLITLNFQNLMA 173
DB 61 EGFYIIHETLQKTODLKLISGNTLFIQDLQPKFLEDAKNFYSAETLITLNFQNLMA 120
QY 174 OKQINDPISQTHKINLLENIDPGTMLANYIFPFAKMKHEPDVNTYSEDFLEKN 233
DB 121 OKQINDPISQTHKINLLENIDPGTMLANYIFPFAKMKHEPDVNTYSEDFLEKN 180
QY 234 SSVVPMFMRSGIYQVGYDDKLSTLIEIPYQKNITAFILPDSGKLKHLKGLQVDTFS 293
DB 181 SSVVPMFMRSGIYQVGYDDKLSTLIEIPYQKNITAFILPDSGKLKHLKGLQVDTFS 240
QY 294 RMTLLSRVVDSVPRLMHTGTFDLKKTLSYIGVSKIFEEHGDLTJLAPRSLKVGAV 353
DB 241 RMTLLSRVVDSVPRLMHTGTFDLKKTLSYIGVSKIFEEHGDLTJLAPRSLKVGAV 300
QY 354 HKELKMDERTEGAGTGAQTLPMETPLVVKIDKPYLLLYSEKIPSVLFGKIIVDFIG 413
DB 301 HKELKMDERTEGAGTGAQTLPMETPLVVKIDKPYLLLYSEKIPSVLFGKIIVDFIG 360
QY 414 K 414
DB 361 K 361

RESULT 14
US-10-037-417-66
Sequence 66, Application US/10037417
Publication No. US20040052806A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernov, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Paturajan, Meera
APPLICANT: Grose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Vermet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomil R
APPLICANT: Sciore, Paul
APPLICANT: Billeman, Karen
APPLICANT: Malyskar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Padigaru, Muralidhara
APPLICANT: Tsapler Jr, Raymond J
APPLICANT: Miller, Charles B
APPLICANT: Bisen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037, 417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260, 018

PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260, 360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272, 411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272, 817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291, 186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303, 231
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/305, 060
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: 60/318, 405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318, 700
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 66
LENGTH: 377
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Serpin
OTHER INFORMATION: Consensus Sequence
US-10-037-417-66

Query Match 39.5%; Score 842; DB 4; Length 377;
Best Local Similarity 43.7%; Pred. No. 2.6e-65;
Matches 163; Conservative 86; Mismatches 118; Indels 6; Gaps 4;

QY 45 AKELARQMDLGFLLKLAFLYNGRNIPLSPISITAFSMLCLGADOSTLDEIKQ--GF 102
DB 5 AKELASADPAFSLYELVEQNDKNIFFSPVISISALMTSLGAGNATATQILEVLGF 64
QY 103 NFRMPKEDLHEGFYIIHETLQKTODLKLISGNTLFIQDLQPKFLEDAKNFYSAET 162
DB 65 NFRMPSAEIHQGFQHLQGLINRPTDGLQTLGNALFVDSLSKLDFLEDSKLYQSEV 124
QY 163 ILTNFQNLMAOKQINDPISQTHKINLLENIDPGTMLANYIFPFAKMKHEPDVNV 222
DB 125 FSVDFSDPEAKQINDVWEKTKQKIDLLKOLDSTVLVIVYIYFKKMKKPEPPEL 184
QY 223 TKERDPLEKNSVYKVMRSGIYQVGYDDKLSTLIEIPYQKNITAFILPDSGKL 280
DB 185 TKERDPLEKNSVYKVMRSGIYQVGYDDKLSTLIEIPYQKNITAFILPDSGKL 244
QY 281 KHLKGLQVDTFSRMTLLSRVVDSVPRLMHTGTFDLKKTLSYIGVSKIFEEHGDLTJ 340
DB 245 KHLKGLQVDTFSRMTLLSRVVDSVPRLMHTGTFDLKKTLSYIGVSKIFEEHGDLTJ 304
QY 341 IAPRSLKVGAVHKLKMDERTEGAGTGAQTLPMETPLVVKIDKPYLLLYSEKIPSV 398
DB 305 IAPRSLKVGAVHKLKMDERTEGAGTGAQTLPMETPLVVKIDKPYLLLYSEKIPSV 364
QY 399 IESVFLGKIIVNP 411
DB 365 IESVFLGKIIVNP 377

RESULT 15
US-10-023-634-87
Sequence 87, Application US/10023634
Publication No. US2003023639A1
GENERAL INFORMATION:
APPLICANT: Shimkets, Richard A
APPLICANT: Coleman, Steven D
APPLICANT: Spytek, Kimberly A
APPLICANT: Ballinger, Robert A
APPLICANT: Guo, Xiaojia
APPLICANT: Tchernov, Velizar T
APPLICANT: Shenoy, Suresh G

APPLICANT: Li, Li
APPLICANT: Ellerman, Karen
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patuturajan, Meera
APPLICANT: Casman, Stacie J
APPLICANT: Boldog, Ferenc
APPLICANT: Gusev, Vladimir Y
APPLICANT: Burgess, Catherine E
APPLICANT: Edinger, Shlomit R
APPLICANT: Gangolli, Beha A
APPLICANT: Malvankar, Uriel M
APPLICANT: Gunther, Erik
APPLICANT: Smithson, Glenda
APPLICANT: Miller, Isabelle
APPLICANT: Gerlach, Valerie
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
FILE REFERENCE: 21402-221
CURRENT APPLICATION NUMBER: US/10/023,634
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/256,025
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: 60/265,163
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: 60/272,929
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/274,864
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/276,688
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,880
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/286,409
PRIOR FILING DATE: 2001-04-25
PRIOR APPLICATION NUMBER: 60/309,246
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/315,600
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 87
LENGTH: 371
TYPE: PRT
ORGANISM: Homo sapiens
US-10-023-634-87

Query Match 39.4%; Score 840; DB 4; Length 371;
Best Local Similarity 43.7%; Pred. No.3.8e-65;
Matches 162; Conservative 86; Mismatches 117; Indels 6; Gaps 4;

QY 47 ELARQNMIDGFKLLKLAFFYNPGRNIFLSPLSISTAFSMLCTGAQDSTLDEIKQ--GFNF 104
DB 1 KLASANADPAFSLYKELVQNPDKNIFSPVSISSALAWLSGAKGNTATQILEVLGFNL 60

QY 105 RCMPEKDLHSGFYHIIHELTOKTQDLKLSIGNTLFDQRLQPOKRFLEDAKNFYSAETTL 164
DB 61 TETSEKEIHQGFQHLQEBLNRPDTGLQTTGNALFVDKSLKLDLEFLBDSKRLYOSEVPS 120

QY 165 TNFQNLMAQKOINDEFISQTHGKINNLEINIDPGTVMILANYIFFRARKHGFDPNVTK 224
DB 121 VDFSPDEBAKQOINDBVEKKTQKIDOLKDLDSDTVLAVNIYTKGKKKPFDEPTE 180

QY 225 EEDFLEKNSVYVPMWFRSGIYQVGDKLSCTILIEPYQKNITA-IFILPDE-GKLRH 282
DB 181 EEDFHYDKTIVKVPWMMQLGTFYFRDEBLNCKVLELPYKGNATSMFLPDPVGVKLEQ 240

QY 283 LEKGQVDTFSPKWTILSRVYDVSVPLAMTGFPLDKTILSTYGVSKIPEEHGDLTKTA 342
DB 241 YEAAISPETLRKLENMERREVELYLPKFSIBGTYDLKDVLANGLITDLFSNQADLSGIS 300

QY 343 PHSRLKVGAEVKAELKMDERGTGGAAGTGAQTLPMETP--LVWKIDKPYLLIYSEKLP 400
DB 301 EBDLKVSAKAVKAVLEVBEGTEAAATGAILVPSLPELEFTADREFFLIYDDPTG 360

QY 401 SVFLGKIYNP 411
DB 361 SILFMGKVVNP 371

Search completed: March 31, 2006, 09:54:36
Job time : 169 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 31, 2006, 09:52:00 ; Search time 24 Seconds
(without alignments)
525.123 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 2130
Sequence: 1 MNPTLGLAIFLAVLTFVKGL.....YSEKIPSEVFLGKIVNPIGK 414

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
1: /SIDS5/ptodata/2/pubpaa/US08_NEM_PUB.pep.*
2: /SIDS5/ptodata/2/pubpaa/US06_NEM_PUB.pep.*
3: /SIDS5/ptodata/2/pubpaa/US07_NEM_PUB.pep.*
4: /SIDS5/ptodata/2/pubpaa/BCT_NEM_PUB.pep.*
5: /SIDS5/ptodata/2/pubpaa/US09_NEM_PUB.pep.*
6: /SIDS5/ptodata/2/pubpaa/US10_NEM_PUB.pep.*
7: /SIDS5/ptodata/2/pubpaa/US11_NEM_PUB.pep.*
8: /SIDS5/ptodata/2/pubpaa/US60_NEM_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	842	39.5	377	7	US-11-019-711-66
2	786	36.9	418	6	US-10-995-561-753
3	786	36.9	418	6	US-10-995-561-754
4	786	36.9	418	6	US-10-995-561-755
5	786	36.9	418	6	US-10-995-561-756
6	786	36.9	418	6	US-10-995-561-757
7	786	36.9	418	6	US-10-995-561-758
8	786	36.9	418	6	US-10-995-561-759
9	785	36.9	418	7	US-11-177-506-27
10	785	36.9	418	7	US-11-183-205-22
11	772.5	36.3	350	7	US-11-019-711-67
12	765.5	35.9	415	7	US-11-044-224-19
13	723.5	34.0	406	6	US-10-995-561-748
14	723.5	34.0	406	6	US-10-995-561-749
15	723.5	34.0	406	6	US-10-995-561-750
16	723.5	34.0	406	6	US-10-995-561-751
17	723.5	34.0	406	6	US-10-995-561-752
18	706	33.1	448	7	US-11-072-512-3380
19	703.5	33.0	417	7	US-11-147-047-39
20	703.5	33.0	423	6	US-10-995-561-794
21	703.5	33.0	423	6	US-10-995-561-795
22	703.5	33.0	448	6	US-10-995-561-793
23	690.5	32.4	417	7	US-11-219-282-23
24	663.5	31.2	403	7	US-11-219-282-24
25	575	27.0	444	6	US-10-131-826A-498

26	575	27.0	444	6	US-10-973-115B-498	Sequence 498, App
27	575	27.0	444	7	US-11-071-580-1	Sequence 1, Appl
28	574	26.9	444	6	US-10-995-561-834	Sequence 834, App
29	574	26.9	444	6	US-10-995-561-835	Sequence 835, App
30	574	26.9	484	6	US-10-995-561-833	Sequence 833, App
31	568	26.7	457	6	US-10-995-561-797	Sequence 797, App
32	479.5	22.5	390	7	US-11-219-282-13	Sequence 13, Appl
33	471.5	22.1	390	7	US-11-019-711-65	Sequence 65, Appl
34	471.5	22.1	390	7	US-11-219-282-12	Sequence 12, Appl
35	467	21.9	366	6	US-10-215-245A-2	Sequence 2, Appl
36	466.5	21.9	376	6	US-10-501-035-283	Sequence 283, App
37	465.5	21.9	374	6	US-10-995-561-668	Sequence 668, App
38	465.5	21.9	374	6	US-10-995-561-669	Sequence 669, App
39	463.5	21.8	376	6	US-10-995-561-844	Sequence 844, App
40	463.5	21.8	376	6	US-10-995-561-846	Sequence 846, App
41	463.5	21.8	380	6	US-10-995-561-847	Sequence 847, App
42	463.5	21.8	390	6	US-10-453-372-554	Sequence 554, App
43	460	21.6	395	6	US-10-453-372-554	Sequence 11, Appl
44	457	21.5	397	7	US-11-219-282-11	Sequence 11, Appl
45	447	21.0	379	7	US-11-219-282-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-11-019-711-66
Sequence 66, Application US/11019711
Publication No. US20060009634A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Alsbrook II, John P
APPLICANT: Tchemnev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Patturajan, Meera
APPLICANT: Grose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine E
APPLICANT: Verneet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciorer, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malyankar, Uriel M
APPLICANT: Rothenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Anderson, David W
APPLICANT: Radigaru, Muralidhara
APPLICANT: Taupler Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Eissen, Andrew J
TITLE OR INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/11/019,711
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: US/10/037,417
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260,360
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/272,411
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 60/272,817
PRIOR FILING DATE: 2001-03-02
PRIOR APPLICATION NUMBER: 60/291,186
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231

;; PRIOR FILING DATE: 2001-07-05
;; PRIOR APPLICATION NUMBER: 60/305,060
;; PRIOR FILING DATE: 2001-07-12
;; PRIOR APPLICATION NUMBER: 60/318,405
;; PRIOR FILING DATE: 2001-09-10
;; PRIOR APPLICATION NUMBER: 60/318,700
;; PRIOR FILING DATE: 2001-09-12
;; NUMBER OF SEQ ID NOS: 227
;; SOFTWARE: Patent In Ver. 2.1
;; SEQ ID NO 66
;; LENGTH: 377
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Serpin
US-11-019-711-66

Query Match 39.5%; Score 842; DB 7; Length 377;
Best Local Similarity 43.7%; Pred. No. 1e-60;
Matches 163; Conservative 86; Mismatches 118; Indels 6; Gaps 4;

QY 45 AKELAQNNDLGRFKLKLAFVNRGRNIFLSPISISTAFSMCLGAQDSTLDEIKQ--GF 102
DB 5 ALKLASANDPAPSLYKELVEQNPDKNIFPSPVSISSALMLSLGAKGNATATQILEVGF 64
QY 103 NFRKMPKDLHGEFHYIHELTKQTDLKLISGNTLFIIDRLQPKRFLEDAKNFYSAET 162
DB 65 NLRTSEAHIGHQFQHLGELNRPDGLQLTGNAFLVDKSLDLDEFLDSRLVQSEV 124
QY 163 ILTNFQNLMAQKQINDPISQKTHGKINLNIENIDGCTMLNANYIFPRARKHEPDNV 222
DB 125 PSVDFSDPEAKQINDVWEKTKQKIKDLKDLDSITVLVNVYIYFKKMKKPPDPPEL 184
QY 223 TKREDFLEKNSVVKVPMFRSGIYQVGYDDKLSCTILIEPYOKNITA--FILLPDE-GKL 280
DB 185 TEEDPHVDKKTIVKPMNQDGFYFPRDEINLCVLEIPYGNATSMFLIPDEVGKL 244
QY 281 KHLKGLQVDTESRMKTLISRNVVDVSPRLHMTGTFDCLKTSLYGVSKIFEEHGLTK 340
DB 245 EQVEALSPETLRKLENNRREVELYLPRFSLGTYDLKQVLAKGIDTDLFENQADLSG 304
QY 341 IAPHRSLKGEAVHAKELKMDERGTEGAAGTGAQTLPMETP--LVVKIDKPYLLIYSEK 398
DB 305 ISEDEDLKYSKAVHKAVLVEDEGTEAATAATGAIIVPRSLPELEFPAURPFLIYDPR 364
QY 399 IPSVLEFLGIKVP 411
DB 365 TGSILFMKGVNVP 377

RESULT 2
US-10-995-561-753
;; Sequence 753, Application US/10995561
;; Publication No. US20050272054A1
;; GENERAL INFORMATION:
;; APPLICANT: CARGILL, Michele et al.
;; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;; TITLE OF INVENTION: DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001559
;; CURRENT APPLICATION NUMBER: US/10/995,561
;; CURRENT FILING DATE: 2004-11-24
;; NUMBER OF SEQ ID NOS: 85702
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 753
;; LENGTH: 418
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-995-561-753

Query Match 36.9%; Score 786; DB 6; Length 418;
Best Local Similarity 42.7%; Pred. No. 4e-56;

Matches 155; Conservative 73; Mismatches 133; Indels 2; Gaps 1;
QY 54 DLGFKLKDAFVNPGRNIFLSPISISTAFSMCLGAQDSTLDEIKQGFNR--KMPKED 111
DB 56 EFAPSLYROLAQSNSNTNIFSPVSIATAPAMLSLSTKADTHDEILEGNFNLTETPEAQ 115
QY 112 LHEGFHYIHELTKQTDKLSIGNTLFIIDRLQPKRFLEDAKNFYSAETIITNFQNTL 171
DB 116 IHEGFQELRLTNQPSQQLTGTGNGLPFSEGLKVDKFLVEDVKLYHSEAFVNGDTE 175
QY 172 MAQKQINDPISQKTHGKINLNIENIDPGYVMLNANYIFPRARKHEPDNVTEEDPFLE 231
DB 176 EAKQKQINDYVEKGTQKQIVDLVKELDORDVFALVNIYIFPKGWERPEYKQDTEEDPHVD 235
QY 232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILIEPYOKNITAIFILPDGSKLHLEKQLOVT 291
DB 236 QATTVKVPMMKLGWNIGHCKKLSWVLMKTLGNATAIIFLPDGGKLOHLENELTHDI 295
QY 292 FSRMKTLLSRNVVDVSPRLHMTGTFDCLKTSLYGVSKIFEEHGLTKIAPHRSLKVG 351
DB 296 ITKFLFENEDRRSASLHLPKLSITGYDLKSVLGQIGITVFSNGADLSGVTEAPLKLK 355
QY 352 AVHKAELKMDERGTEGAAGTGAQTLPMETPVLVVKIDKPYLLIYSEKISVLEFLGIKVP 411
DB 356 AVHKAVALTIDERGTEGAAGMFLAIPMSIPPEYKFNKPPVFLMIENQTSPLFMKGVNVP 415
QY 412 ICK 414
DB 416 TQK 418

RESULT 3
US-10-995-561-754
;; Sequence 754, Application US/10995561
;; Publication No. US20050272054A1
;; GENERAL INFORMATION:
;; APPLICANT: CARGILL, Michele et al.
;; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
;; TITLE OF INVENTION: DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001559
;; CURRENT APPLICATION NUMBER: US/10/995,561
;; CURRENT FILING DATE: 2004-11-24
;; NUMBER OF SEQ ID NOS: 85702
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 754
;; LENGTH: 418
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-995-561-754

Query Match 36.9%; Score 786; DB 6; Length 418;
Best Local Similarity 42.7%; Pred. No. 4e-56;
Matches 155; Conservative 73; Mismatches 133; Indels 2; Gaps 1;
QY 54 DLGFKLKDAFVNPGRNIFLSPISISTAFSMCLGAQDSTLDEIKQGFNR--KMPKED 111
DB 56 EFAPSLYROLAQSNSNTNIFSPVSIATAPAMLSLSTKADTHDEILEGNFNLTETPEAQ 115
QY 112 LHEGFHYIHELTKQTDKLSIGNTLFIIDRLQPKRFLEDAKNFYSAETIITNFQNTL 171
DB 116 IHEGFQELRLTNQPSQQLTGTGNGLPFSEGLKVDKFLVEDVKLYHSEAFVNGDTE 175
QY 172 MAQKQINDPISQKTHGKINLNIENIDPGYVMLNANYIFPRARKHEPDNVTEEDPFLE 231
DB 176 EAKQKQINDYVEKGTQKQIVDLVKELDORDVFALVNIYIFPKGWERPEYKQDTEEDPHVD 235
QY 232 KNSSVKVPMMFRSGIYQVGYDDKLSCTILIEPYOKNITAIFILPDGSKLHLEKQLOVT 291
DB 236 QATTVKVPMMKLGWNIGHCKKLSWVLMKTLGNATAIIFLPDGGKLOHLENELTHDI 295
QY 292 FSRMKTLLSRNVVDVSPRLHMTGTFDCLKTSLYGVSKIFEEHGLTKIAPHRSLKVG 351

Db 296 ITRKLENERDRSRASLHPKLSITGTVDLKSGLGGLTKVPSNGADLSGVTEBAPLKLKSK 355
Qy 352 AVHKAELKMDERGTGAAGTGAOTLPMETPLVYKIDKPYLLIYSEKIPSTLPIGKIYVP 411
Db 356 AVHKAVALTIDKGTBAAGAMFLBAIPMSIPPEVKFNPFFVLMLEQNTSKPLFWGKVVP 415
Qy 412 IGR 414
Db 416 TOK 418

RESULT 4
US-10-995-561-755
; Sequence 755, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FaestSeq for Windows Version 4.0
; SEQ ID NO 755
; LENGTH: 418
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-995-561-755

Query Match 36.9%; Score 786; DB 6; Length 418;
Best Local Similarity 42.7%; Pred. No. 4e-56;
Matches 155; Conservative 73; Mismatches 133; Indels 2; Gaps 1;
Qy 54 DLGPKLKLKLAFTNPGNIFLSPISISTAPSMCLGAODSTLDEIKGPNFR--KMPBKD 111
Db 56 EFAPSLYRQLAHSNSTNIFSPVSITAFAMSLGTRKADTHDEILGLNPNLFEIPEAQ 115
Qy 112 LHGFGFYIHELTKQTDKLSTGNTLFIQRLQPKRFLBDANFYSAEITLTFNPNLE 171
Db 116 IHGFGFLTLTLNQPDSQLTGTNGFLPSBGLKYDKFLBDVYKLYHSEAFYVNFQDTE 175
Qy 172 MAQKQINDFISQKTHGKINNLIENIDPGYMLLANTYIFPARWGHBDPNTKEDEFLB 231
Db 176 EAKQINDYVEKGTGKIYDLVKELDRDYFALVNIYFFPKMERPEVYKDEEDFHYD 235
Qy 232 KNSSVKVPMMFRSGIYGVYDDKLSCTILBIPYOKNTAIFILPDEGKLKLEGLQVDT 291
Db 236 QATTVKVPMMKRLGMFNIOHCKLSSWVLMKYLGNATATLFFLPDEGKLQHLENELTHDI 295
Qy 292 FSRWKTILSRVVDVSPRLHMTGTPDKTSLTIGVSKIPEEHGDLTKLAPHRSKLVGE 351
Db 296 ITRKLENERDRSRASLHPKLSITGTVDLKSGLGGLTKVPSNGADLSGVTEBAPLKLKSK 355
Qy 352 AVHKAELKMDERGTGAAGTGAOTLPMETPLVYKIDKPYLLIYSEKIPSTLPIGKIYVP 411
Db 356 AVHKAVALTIDKGTBAAGAMFLBAIPMSIPPEVKFNPFFVLMLEQNTSKPLFWGKVVP 415
Qy 412 IGR 414
Db 416 TOK 418

RESULT 5
US-10-995-561-756
; Sequence 756, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FaestSeq for Windows Version 4.0
; SEQ ID NO 756
; LENGTH: 418
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-995-561-756

Query Match 36.9%; Score 786; DB 6; Length 418;
Best Local Similarity 42.7%; Pred. No. 4e-56;
Matches 155; Conservative 73; Mismatches 133; Indels 2; Gaps 1;
Qy 54 DLGPKLKLKLAFTNPGNIFLSPISISTAPSMCLGAODSTLDEIKGPNFR--KMPBKD 111
Db 56 EFAPSLYRQLAHSNSTNIFSPVSITAFAMSLGTRKADTHDEILGLNPNLFEIPEAQ 115
Qy 112 LHGFGFYIHELTKQTDKLSTGNTLFIQRLQPKRFLBDANFYSAEITLTFNPNLE 171
Db 116 IHGFGFLTLTLNQPDSQLTGTNGFLPSBGLKYDKFLBDVYKLYHSEAFYVNFQDTE 175
Qy 172 MAQKQINDFISQKTHGKINNLIENIDPGYMLLANTYIFPARWGHBDPNTKEDEFLB 231
Db 176 EAKQINDYVEKGTGKIYDLVKELDRDYFALVNIYFFPKMERPEVYKDEEDFHYD 235
Qy 232 KNSSVKVPMMFRSGIYGVYDDKLSCTILBIPYOKNTAIFILPDEGKLKLEGLQVDT 291
Db 236 QATTVKVPMMKRLGMFNIOHCKLSSWVLMKYLGNATATLFFLPDEGKLQHLENELTHDI 295
Qy 292 FSRWKTILSRVVDVSPRLHMTGTPDKTSLTIGVSKIPEEHGDLTKLAPHRSKLVGE 351
Db 296 ITRKLENERDRSRASLHPKLSITGTVDLKSGLGGLTKVPSNGADLSGVTEBAPLKLKSK 355
Qy 352 AVHKAELKMDERGTGAAGTGAOTLPMETPLVYKIDKPYLLIYSEKIPSTLPIGKIYVP 411
Db 356 AVHKAVALTIDKGTBAAGAMFLBAIPMSIPPEVKFNPFFVLMLEQNTSKPLFWGKVVP 415
Qy 412 IGR 414
Db 416 TOK 418

RESULT 6
US-10-995-561-757
; Sequence 757, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FaestSeq for Windows Version 4.0
; SEQ ID NO 757
; LENGTH: 418
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-995-561-757

Query Match 36.9%; Score 786; DB 6; Length 418;
Best Local Similarity 42.7%; Pred. No. 4e-56;
Matches 155; Conservative 73; Mismatches 133; Indels 2; Gaps 1;
Qy 54 DLGPKLKLKLAFTNPGNIFLSPISISTAPSMCLGAODSTLDEIKGPNFR--KMPBKD 111
Db 56 EFAPSLYRQLAHSNSTNIFSPVSITAFAMSLGTRKADTHDEILGLNPNLFEIPEAQ 115
Qy 112 LHGFGFYIHELTKQTDKLSTGNTLFIQRLQPKRFLBDANFYSAEITLTFNPNLE 171


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Db      116 IHGFEQLRTLTLPDPSQQLTGTNGFLFSEGLKYDKLFEDVKLYHSEAFVTFEGDTE 175
      172 MAQKOINDPISQTHGKINNLINIDPGTMLLANYIFPRAKWHEDPVTKEEDFFLE 231
      176 EAKKOINDYVEKGTQKIDVLVEKLDRTVPALVNYIFFGKWERPEVQDTEEDFHVD 235
Qy      232 KNSSVKVPMMFSGIYQVGDYDKLSTLIEIPYOKNITAIFFLPDEGKLHLEKGLQVDT 291
      236 QATTVKVPMMKRLGMFNIGHCKLSSWVLMKTLGNATAIFFLPDEGKLQHLENELTHDI 295
Qy      292 FSRMKTLLSRVVDVSPRLHMTGTFDLPKKTLSYIGVSKIFEEHGLTKIAPHRSKLVGE 351
      296 ITKFLENEDRRASLHLPKLSITGYDKSVLGQLGITTKVFSNGADLSGVTBEAPLKSK 355
Qy      352 AVHKAELKMDERGTEGAAGTGLPMTETPLVVKIDKPYLLIYSEKIPSVLFLKTVNP 411
      356 AVHKAVALTIDERGTEAAGMFLPAIPMSIPPEVKPKPFVFLMIEDQNTSPLEFMGKVNP 415
Db      412 IGR 414
      416 TQK 418

```

```

RESULT 7
US-10-995-561-758
; Sequence 758, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 758
; LENGTH: 418
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-995-561-758

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Query Match      36.9%; Score 786; DB 6; Length 418;
Best Local Similarity 42.7%; Pred. No. 4e-56;
Matches 155; Conservative 73; Mismatches 133; Indels 2; Gaps 1;

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Qy      54 DLGFKLLKGLAFYNPGRNIFLSPISITAFSMCLGAQDSTLDEIKQGNFR--KMPKRD 111
      56 EFAPSLYRQLAHQSNSTNIFSPVSITAFAMLSLGTAKDTHDEILEGNFNLTEIPEAQ 115
Db      112 LHGFFYIHELTQKTDKLSIGNTLFIQDRLQPORKELEDAKNYSATETILTNPQNE 171
      116 IHGFEQLRTLTLPDPSQQLTGTNGFLFSEGLKYDKLFEDVKLYHSEAFVTFEGDTE 175
Qy      172 MAQKOINDPISQTHGKINNLINIDPGTMLLANYIFPRAKWHEDPVTKEEDFFLE 231
      176 EAKKOINDYVEKGTQKIDVLVEKLDRTVPALVNYIFFGKWERPEVQDTEEDFHVD 235
Db      232 KNSSVKVPMMFSGIYQVGDYDKLSTLIEIPYOKNITAIFFLPDEGKLHLEKGLQVDT 291
      236 QATTVKVPMMKRLGMFNIGHCKLSSWVLMKTLGNATAIFFLPDEGKLQHLENELTHDI 295
Qy      292 FSRMKTLLSRVVDVSPRLHMTGTFDLPKKTLSYIGVSKIFEEHGLTKIAPHRSKLVGE 351
      296 ITKFLENEDRRASLHLPKLSITGYDKSVLGQLGITTKVFSNGADLSGVTBEAPLKSK 355
Db      352 AVHKAELKMDERGTEGAAGTGLPMTETPLVVKIDKPYLLIYSEKIPSVLFLKTVNP 411
      356 AVHKAVALTIDERGTEAAGMFLPAIPMSIPPEVKPKPFVFLMIEDQNTSPLEFMGKVNP 415
Qy      412 IGR 414
      416 TQK 418

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Db      416 TQK 418

RESULT 8
US-10-995-561-759
; Sequence 759, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 759
; LENGTH: 418
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-995-561-759

```

```

Query Match      36.9%; Score 786; DB 6; Length 418;
Best Local Similarity 42.7%; Pred. No. 4e-56;
Matches 155; Conservative 73; Mismatches 133; Indels 2; Gaps 1;

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```

Qy      54 DLGFKLLKGLAFYNPGRNIFLSPISITAFSMCLGAQDSTLDEIKQGNFR--KMPKRD 111
      56 EFAPSLYRQLAHQSNSTNIFSPVSITAFAMLSLGTAKDTHDEILEGNFNLTEIPEAQ 115
Db      112 LHGFFYIHELTQKTDKLSIGNTLFIQDRLQPORKELEDAKNYSATETILTNPQNE 171
      116 IHGFEQLRTLTLPDPSQQLTGTNGFLFSEGLKYDKLFEDVKLYHSEAFVTFEGDTE 175
Qy      172 MAQKOINDPISQTHGKINNLINIDPGTMLLANYIFPRAKWHEDPVTKEEDFFLE 231
      176 EAKKOINDYVEKGTQKIDVLVEKLDRTVPALVNYIFFGKWERPEVQDTEEDFHVD 235
Db      232 KNSSVKVPMMFSGIYQVGDYDKLSTLIEIPYOKNITAIFFLPDEGKLHLEKGLQVDT 291
      236 QATTVKVPMMKRLGMFNIGHCKLSSWVLMKTLGNATAIFFLPDEGKLQHLENELTHDI 295
Qy      292 FSRMKTLLSRVVDVSPRLHMTGTFDLPKKTLSYIGVSKIFEEHGLTKIAPHRSKLVGE 351
      296 ITKFLENEDRRASLHLPKLSITGYDKSVLGQLGITTKVFSNGADLSGVTBEAPLKSK 355
Db      352 AVHKAELKMDERGTEGAAGTGLPMTETPLVVKIDKPYLLIYSEKIPSVLFLKTVNP 411
      356 AVHKAVALTIDERGTEAAGMFLPAIPMSIPPEVKPKPFVFLMIEDQNTSPLEFMGKVNP 415
Qy      412 IGR 414
      416 TQK 418

RESULT 9
US-11-177-506-27
; Sequence 27, Application US/11177506
; Publication No. US20060029956A1
; GENERAL INFORMATION:
; APPLICANT: Beyer, Wayne F.
; APPLICANT: Venetta, John W.
; APPLICANT: Groelke, John M.
; APPLICANT: Blaesius, Rainer H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DETECTION OF OVARIAN DISEASE
; FILE REFERENCE: 46143/294851
; CURRENT APPLICATION NUMBER: US/11/177,506
; CURRENT FILING DATE: 2005-07-08
; PRIOR APPLICATION NUMBER: 60/586,856
; PRIOR FILING DATE: 2004-07-09

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; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 27
; LENGTH: 418
; TYPE: prt
; ORGANISM: Homo sapiens
; OS-11-177-506-27

```

Query Match	36.9%	Score 785;	DB 7;	Length 418;
Beet Local Similarity	42.7%	Pred. No. 4.9e-56;		
Matches 155;	Conservative 73;	Mismatches 133;	Indels 2;	Gaps 1;

[illegible]

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RESULT 10
US-11-183-205-22
Sequence 22, Application US/11183205
Publication No. US20060030521A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Bove, Caryn
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
FILE REFERENCE: 040853-01-5052-US01
CURRENT FILING DATE: US/11/183,205
PRIORITY FILING DATE: 2005-07-15
PRIORITY FILING DATE: US 11/183,205
PRIORITY FILING DATE: 2005-07-15
PRIORITY FILING DATE: US 60/334,233
PRIORITY FILING DATE: 2001-11-28
PRIORITY FILING DATE: US 60/334,301
PRIORITY FILING DATE: 2001-11-28
PRIORITY FILING DATE: US 60/387,292
PRIORITY FILING DATE: 2002-06-07
PRIORITY FILING DATE: US 60/391,777
PRIORITY FILING DATE: 2002-06-25
PRIORITY FILING DATE: US 60/396,594
PRIORITY FILING DATE: 2002-07-17
PRIORITY FILING DATE: US 60/404,249
PRIORITY FILING DATE: 2002-08-16
PRIORITY FILING DATE: US 60/407,527
PRIORITY FILING DATE: 2002-08-28

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? PRIOR APPLICATION NUMBER: PCT/US2002/032266
? PRIOR FILING DATE: 2002-10-09
? PRIOR APPLICATION NUMBER: US 10/287,994
? PRIOR FILING DATE: 2002-11-05
? NUMBER OF SEQ ID NOS: 62
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 22
?
? LENGTH: 418
?
? TYPE: prt
? ORGANISM: Homo sapiens
? US-11-183-205-22

```

Query Match	36.9%;	Score 785;	DB 7;	Length 418;
Best Local Similarity	42.7%;	Pred. NO. 4.9e-56;		
Matches 155; Conservative	73;	Mismatches 133;	Indels 2;	Gaps 1

[illegible]

RESULT 11
US-11-019-711-67

Sequence 67, Application US/110197111
Publication No. US2006009634A1

GENERAL INFORMATION:

APPLICANT: Akhuda, Ramesh
APPLICANT: Albrook II, John P
APPLICANT: Tchernov, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Paturjanjan, Meera
APPLICANT: Grosse, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burgess, Catherine B
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Gorman, Linda
APPLICANT: Edinger, Shlomit R
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: Malayankar, Utiel M
APPLICANT: Rotenberg, Mark
APPLICANT: Stone, David J
APPLICANT: Boldog, Ferenc L
APPLICANT: Guo, Xiaojia
APPLICANT: Shenoy, Suresh G
APPLICANT: Andersson, David W
APPLICANT: Padigaru, Muralidhara

```
/ APPLICANT: Taupier Jr, Raymond J
/ APPLICANT: Miller, Charles E
/ APPLICANT: Eissen, Andrew J
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-235
/ CURRENT APPLICATION NUMBER: US/11/019,711
/ CURRENT FILING DATE: 2004-12-21
/ PRIOR APPLICATION NUMBER: US/10/037,417
/ PRIOR FILING DATE: 2002-09-20
/ PRIOR APPLICATION NUMBER: 60/260,018
/ PRIOR FILING DATE: 2001-01-05
/ PRIOR APPLICATION NUMBER: 60/260,360
/ PRIOR FILING DATE: 2001-01-08
/ PRIOR APPLICATION NUMBER: 60/272,411
/ PRIOR FILING DATE: 2001-02-28
/ PRIOR APPLICATION NUMBER: 60/272,817
/ PRIOR FILING DATE: 2001-03-02
/ PRIOR APPLICATION NUMBER: 60/291,186
/ PRIOR FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: 60/303,231
/ PRIOR FILING DATE: 2001-07-05
/ PRIOR APPLICATION NUMBER: 60/305,060
/ PRIOR FILING DATE: 2001-07-12
/ PRIOR APPLICATION NUMBER: 60/318,405
/ PRIOR FILING DATE: 2001-09-10
/ PRIOR APPLICATION NUMBER: 60/318,700
/ PRIOR FILING DATE: 2001-09-12
/ NUMBER OF SEQ ID NOS: 227
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 67
/ LENGTH: 360
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Serpin
/ OTHER INFORMATION: Consensus Sequence
US-11-019-711-67
```

Query Match 36.3%; Score 772.5; DB 7; Length 360;

Best Local Similarity 41.9%; Pred. No.4,1e-55; Matches 151; Conservative 85; Mismatches 119; Indels 5; Gaps 4;

```
QY 57 FTLKLLKLAAYNPGRNIFLSPISITAFSMCLGAQDSTLDEIKQ--GFNFRKAPBEKOLHE 114
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 POLYKELAKESPDKNIFSPVISISALAMSLGAKSTATQILEVGFNLTERSEADINQ 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 115 GHHYIIHETLOKTQDLSIGNTLFTDQLOPQKFLBDKAPFYSMETILTNFQN-LEMA 173
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 GEOHLHLHLNRPDKQLQRTANALFYDKSLKLDSEFLBDVKCLYGAEVOSVDFPAEERA 120
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 174 OKOINDFISOKTHGKINNLINENIDPGTWMLANYIFFRARWKHEPDPNTYKEDPFLBKN 233
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 KQOINDWVKKTKQCKIKDLISDIDPTRLVNLNATFFKGMKTPPDENTRESDFYDET 180
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 234 SSVKQVPMWRSG-IVGVYDDKLSCTILBIPYOKNTAIFILPDEBGLKHLKGLQVDTF 292
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 181 TTVKQVPMWQGTGRTFPRYGRDEBLNCOVLELPYKGNASMLIILPDEGLFTEVKALPPTLU 240
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 293 SSWKTLISRRVVDVSPRLHMTGTFPLKKTLSITIGYSKIFEEBGGDTIKIAPHSKLVGA 352
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 241 KMTVSLTATRSVELYLPKFLBELSYDLKQVLEGLGTTDFSNKADISGISBBDLVKYSKV 300
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 353 VHKAEKLMDEGRTEGAAGTQTLPMWE-TPLVYKIDKPYLLIYSEKISVLFGLKIYNP 411
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 301 VHKAFLEVNBEETGAALAGTIVIPKSLPPEPFKARPPFLIRDPNPTGISILFMGKVPNP 360
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 12

US-11-044-224-19

/ Sequence 19, Application US/11044224

/ Publication No. US20060040867A1

/ GENERAL INFORMATION:

/ APPLICANT: Shapito, Ireland

```
/ TITLE OF INVENTION: Inhibitors of Serine Protease Activity and Their Use in Methods
/ TITLE OF INVENTION: and Compositions for Treatment of Bacterial Infections
/ FILE REFERENCE: 114232,107
/ CURRENT APPLICATION NUMBER: US/11/044,224
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: 60/123,167
/ PRIOR FILING DATE: 1999-03-05
/ PRIOR APPLICATION NUMBER: 60/137,795
/ PRIOR FILING DATE: 1999-06-03
/ PRIOR APPLICATION NUMBER: 09/518,098
/ PRIOR FILING DATE: 2000-03-03
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 19
/ LENGTH: 415
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-11-044-224-19
```

Query Match 35.9%; Score 765.5; DB 7; Length 415;

Best Local Similarity 42.6%; Pred. No.1,8e-54; Matches 155; Conservative 72; Mismatches 130; Indels 7; Gaps 3;

```
QY 54 DLGFKLLKLAAYNPGRNIFLSPISITAFSMCLGAQDSTLDEIKQGFNFR--KMPKED 111
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 56 EFAPSLYRQLA---STNIFSPVISIATAPAMLSIGTKADTDEILDEIGLNFILTEIPBAQ 111
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 112 LHEGHHYIIHETLOKTQDLSIGNTLFTDQLOPQKFLBDKAPFYSMETILTNFQNLE 171
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 112 IHGFGELLRLTNQPDQQLTGTGNGLFISEGDKVDKFLBDVKCLYHSEAAFTVNGTDE 171
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 172 MAOKQ-INDFISOKTHGKINNLINENIDPGTWMLANYIFFRARWKHEPDPNTYKEDPFL 230
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 172 EAKKQITINDYVERKQOGKIVDLVKELDRDTVALNNTIFFKGMKRPFEVKTDEEDFYV 231
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 231 EKNSSYKVPWMPFRSGIYGVYDDKLSCTILBIPYOKNTAIFILPDEBGLKHLKGLQVD 290
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 232 DQVTVKVPWMPRLGWFNIQHCCKLSWVLKMKYLGNAATPAIFLPDEGKLOHLENELTHD 291
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 291 TTSRWKTLISRRVVDVSPRLHMTGTFDKKTLSTIYGSKIPEBHDDTKIAPHSKLVG 350
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 292 ITTKLENEBRRSASLHPKLSITGYDLSVGLGQIGTVPKNSGADISGVTEBAPDKLS 351
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 351 EAVHKAELKMDRGTEGAAGTQTLPMETPLVYKIDKPYLLIYSEKIPSYLFLGLKIYN 410
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 352 KAVHKAVALTIDKGTGAAGAMFLBAPMSIPPEVYENKPFVLMIEQNTKSLFPMCKVYN 411
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 411 PTGK 414
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 412 PTQK 415
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 13

US-10-995-561-748

/ Sequence 748, Application US/10995561

/ Publication No. US20050272054A1

/ GENERAL INFORMATION:

/ APPLICANT: CARGILL, Michele et al.

/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

/ TITLE OF INVENTION: DETECTION AND USES THEREOF

/ FILE REFERENCE: CL001559

/ CURRENT APPLICATION NUMBER: US/10/995,561

/ CURRENT FILING DATE: 2004-11-24

/ NUMBER OF SEQ ID NOS: 85702

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 748

/ LENGTH: 406

/ TYPE: PRF

/ ORGANISM: Homo sapiens

US-10-995-561-748

Query Match 34.0%; Score 723.5; DB 6; Length 406;

Best Local Similarity 37.0%; Pred. No. 4.6e-51;
Matches 153; Conservative 88; Mismatches 156; Indels 17; Gaps 6;

Qy	7	LAIFP----	AVLLTVGKLPSPFS	PRYKALSEYQKQKMAELARQNMWDGFKLLKTL	63
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	1	MOLFLLCLVLSPQASL	HRHHPRMKGRV----	DHVGATVAPDSRRDFTFDLYRAL	56
		:	:	:	:
		:	:	:	:
		:	:	:	:
Qy	64	AFYNGRNI	FLSPLSISTAFSM	LCIQAODSTLDEIKO--GFNRKMPKEXOLDHGFIYIH	121
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	57	ASAPSGSIFESPVS	ISMSLMTSLCAGASSTWQ	ILEGLNLQKSEKELHGFQQLQ	116
		:	:	:	:
		:	:	:	:
		:	:	:	:
Qy	122	ELTQKTDOLKLSIGNTL	PIDORLOPRKFL	LEDAKAPYSKETITLTNQNLEMAOKOINDFI	181
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	117	ELNDRDGFQSLSGNAL	FTDVLVDDI	ODTVSAMKTYLADTFEPTNPRDSAGAKOINDYV	176
		:	:	:	:
		:	:	:	:
		:	:	:	:
Qy	182	SOKTGRKNNIN	IENTDPCVTMLTANYI	FEPRAKHGFEDPNVTGEEDPFLKXNSVAVPVM	241
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	177	AKQTKGKLVDDLK	KNDSNAVVMWYI	IFPAKMEITSFHNKGTQEOBPYISETVVRPVM	236
		:	:	:	:
		:	:	:	:
		:	:	:	:
Qy	242	FRSGIYQVGYDDKLS	CTILIEPQKNI	TAFILPDEGKLKHLKGLQVDTFSKMKTLISR	301
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	237	SREDQYHLLDRNLS	SCRVVGVPGNATL	FLIPSEGRKQOYENGLSSEKTLRKMLMFPKX	296
		:	:	:	:
		:	:	:	:
		:	:	:	:
Qy	302	RVDVSVARLMMTG	TFDLKTLSTYGVSK	IFEEHGDULTIAPRSLKAGBANYKAEIKOD	361
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	297	QOLEIYLPKFS	IEGSEYOLEKVL	PSLGISNVFTSHDLSGISNHSNIOQESMWHAKAVEAD	356
		:	:	:	:
		:	:	:	:
		:	:	:	:
Qy	362	ERTEGAGAGTG	----	OTLPMETPLVYKDKDYLLIYSEKPIPSVFLIKIYVP	411
		:	:	:	:
		:	:	:	:
		:	:	:	:
Db	357	ESGTRBAATAATG	ITPFRSARLMSQRLV	FNRPPLMETVDN--NNILFLKQVNDP	406

RESULT 14
US-10-995-561-749

```

: Sequence 749, Application US/10995561
: Publication No. US20050272054A1
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele et al.
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
: TITLE OF INVENTION: DETECTION AND USES THEREOF
: FILE REFERENCE: CL001559
: CURRENT APPLICATION NUMBER: US/10/995,561
: CURRENT FILING DATE: 2004-11-24
: NUMBER OF SEQ ID NOS: 85702
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 749
: LENGTH: 406
: TYPE: PR1
: ORGANISM: Homo sapiens
: IS-10-995-561-749

```

Query Match	Score	DB 6	Length
34.0%	723.5	406	

Matches 153; Conservative 88; Mismatches 156; Indels 17; Gaps 6;

Dy 7 LAFL---AVLLTYKGLKPSPSPRYKALSEVGCMQRMAKELARQNMDLGFKLKKL 63
::: ||| :: | : : |
Db 1 MQLFLLCLVLTSPQGASLRHHHPREMKRVE---DLHGATVA PSSRRDFTFDLYTAL 56

Dy 64 AFNPGRNPLSPSLISTAFSMCLGAQDSLDEIK--GFPFRKMEKDLHGFFHYI IH 121
Db 57 ASAAPSGSIPFSPISMSLMTLGAGSFTWQLIEGLGNLTQKSEKEKLHFGQDLD 116

```
Dy      122 ELQKQTQDGLSIGITTLPIQRQLQPKRPLEDAKNFYSAEITLTNPGULEMAQQINDFI 181
        |||::||| | : | : | : ||||:
Db      117 ELNQPRDGQSLSTGNALFTDLVDVLDQDTFSAMKITLYLADPEPTNFRDSAGAMQINDYV 176
```

Qy 182 SÖKTHGKINNLIENTDPCTWLLANYPFRARWKHEPBDPNVTKKEBDFLEKUSSVKYPM 2411
::: ||| :::: | :::: |||| :::: | :::: : ||||
Db 177 AKORRGKIYDLKNLSNAVVTIMAVTFFKAWEETSBNHKGNOFOEPVLTSEFWARVUM 216

242 FRSGIYQVGYDKUSTILEIPYQKNITAFILPDEGKLKHEKGLVDTPSRWKTLLSR 3011

```

Db      237 SNEEDQYHILDPNLSRCRVGVVPOGNATYLFILPSGCKQOJENGSEKTLRMLKMFKK 2366
Qy      302 RVDVSVPLAHMTGTFEDLKKTLSTYIGVSKIFEEHGDLYIAIPRLSLKVGSAVHKAELKOD 3611
      297 RQLEAYLPLPFSTIEGSGYOLEKVPISLGISINVFPSTHDLDSGISNHSNTOVSMVHKAVEVD 3566
Db      362 EKGTEGAAGTGA---QTLPMETPLVWKIDKDYPLLIIYSEKIPSYVFLGRIYVP 411
      357 ESGTAAAAATGIIFFRSARLNSQGLV-FNRFFLMEIYVN--NILEFLGKVRNP 406

```

RESULT 15
US-10-995-561-750

```

/ Sequence 750, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ TITLE OF INVENTION: DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 750
/ LENGTH: 406
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-995-561-750

```

Query Match 34.0%; Score 723.5; DB 6; Length 406;

Matches 153; Conservative 88; Mismatches 156; Indels 17; Gaps 6;

7 LAIFL---AVLLTVKGLLKPSFSPRNYKALSEVQGWKQRMAMAKELARQNMDLGFKLLKL 63

Db 1 MQLFLLCLVLLSPQASLRRHHPREMKRVE----DLNKGATVAPSSRRPFTFDLYRAL 56

Qy 64 AFYNGRNIFLSPLSISTAFSMLCTGAODSTLDEIKQ--GENFRKNEKDLHEGFHYI 121

Db 5' ASAA⁺PSQ⁺IFPSPV⁺ISM⁺SLAM⁺LSGAGS⁺STK⁺MQ⁺LEGGL⁺INT⁺QK⁺SS⁺SEKEL⁺HRG⁺FO⁺LLQ 116

Qy 122 ELTQ⁺TKD⁺KL⁺SG⁺NT⁺LFID⁺Q⁺LPQ⁺RK⁺FL⁺EDAK⁺NY⁺SA⁺ET⁺LT⁺NT⁺QNL⁺EMA⁺Q⁺IND⁺FI 181

Db 117 ELANGPRDGEQLSTLGNALFTFDLVLVDLQDTEVSAMKLYLADTEPTNPRDRDSACAMKQINDYV 176

Qy 182 SQRTHGKINNLINLENIIDPGTYMLLANYIIFPRARKGIEFDPNVYTKBEDFLEKNSSVKYRPM 241

Db 177 AKQKRGKIDVLLKNLDSNVAIVMANYIIFPAKMETSFNNHKTQEOEDFVYVTSIVRVRPM 236

Qy 242 FRSGIYQVGVDDKSLTILEIPYQKNITAFILPREGKLNLEKGIQVDTFSRWKILLR 301

Db 23 SREDOYHYLDRLNLSRWWGVPOGNATALFILPBGKMOQVENGISEKTRIKWLMFKK 296

Gy 302 RVVDVSVBPLMHGTFDLKKTLSYGVSKIPEEHDLTKLAPHRSLKVGAEVHKABKMD 361

DB 297 RQLELYLPKPSIEGSYOLEKVLPSIGISINVFETSHADLSGINSNHSNTQVSEMHKAAVEVD 356

QY 362 ERREGGAAGTGA-----QTLPMETPLVVKIDKPYLLLIYSEKIPSVLEFGKLVNP 411

Search completed: March 31, 2006, 09:55:06
Job time : 25 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2006, 09:54:55 ; Search time 221.073 Seconds
(without alignments)
822.818 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 414
Sequence: 1 MNPTLGIAIFLAVLITVKG.....YSEKIPSVLFGKIVNPIGR 414

Scoring table: OLIGO4
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 15

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

- Database : A_Geneseq_21.*
- 1: geneseqp1980s.*
 - 2: geneseqp1990s.*
 - 3: geneseqp2000s.*
 - 4: geneseqp2001s.*
 - 5: geneseqp2002s.*
 - 6: geneseqp2003as.*
 - 7: geneseqp2003bs.*
 - 8: geneseqp2004s.*
 - 9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB	ID
1	414	100.0	414 4 AAU05754
2	414	100.0	414 4 AAO04885
3	414	100.0	414 6 ADA57300
4	414	100.0	414 6 ADA41179
5	414	100.0	414 8 ADN05952
6	414	100.0	415 3 AAY86217
7	414	100.0	415 6 ABO53360
8	353	85.3	414 4 AAM78898
9	310	74.9	358 4 AAU05759
10	181	43.7	431 4 ABB11832
11	181	43.7	431 4 AAM79882
12	129	31.2	140 4 AAM70426

ALIGNMENTS

RESULT 1
AAU05754
ID AAU05754 standard; protein; 414 AA.
XX AC AAU05754;
XX DT 24-OCT-2001 (first entry)

XX DE Human NOV7 polypeptide.
XX KW Human, NOV7, AL132990 B; fertility disorder; spermatogenesis; cardiac;
KW cytosolic; immunomodulatory; antiproliferative; antidiabetic;
KW cell proliferation; cancer; diabetic retinopathy; angiogenic disorder;
KW pulmonary disorder; haematopoietic disorder; immunological disorder;
KW inflammatory disorder; tumour related disorders; emphysema; cirrhosis;
KW wound healing; gene therapy.
XX OS Homo sapiens.
XX PN W0200149729-A2.
XX PD 12-JUL-2001.
XX PF 05-JAN-2001; 2001KO-US000299.
XX PR 06-JAN-2000; 2000US-0174724P.
XX PR 11-JAN-2000; 2000US-0175434P.
XX PR 11-JAN-2000; 2000US-0175488P.
XX PR 12-JAN-2000; 2000US-0175696P.
XX PR 12-JAN-2000; 2000US-0175743P.
XX PR 13-JAN-2000; 2000US-0175819P.
XX PR 07-AUG-2000; 2000US-0223524P.
XX PR 04-JAN-2001; 2001US-00755665.
XX PA (CURA-) CURAGEN CORP.
XX PI Prayaga SK, Majumder K, Taillon BE, Spaderna SK, Spytek KA;
XX PI MacDougall J;
XX DR WPI: 2001-418356/44.
XX DR N-PSDB; AAS10874.
XX PS Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful
XX PT for treating a syndrome associated with a NOVX-associated disorder, e.g.
XX PT cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or
XX PT pulmonary disorder.
XX PS Claim 1, Page 32, 144pp; English.
XX CC The invention relates to nucleic acids encoding NOVX (X being an integer
XX CC from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
XX CC useful in diagnosing, treating or manufacturing a medicament for a
XX CC disease or disorder associated with NOVX e.g. cell proliferation (cancer
XX CC and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
XX CC disorders (e.g. of spermatogenesis), haematopoietic, immunological,
XX CC inflammatory and tumour related disorders, emphysema, cirrhosis, wound
XX CC healing. NOVX nucleic acids are also useful in gene therapy. They are
XX CC also used for screening for a modulator of activity or of latency or
XX CC predisposition to a NOVX-associated disorder. They are also useful for
XX CC determining the presence of or predisposition to a NOVX-associated
XX CC disorder. The present sequence represents NOV7 (AL132990 B), which has
XX CC sequence homology to an unidentified human secreted protein (HMHGUS54)
XX CC and to alpha anti-trypsin
XX SO Sequence 414 AA;
QY Query Match 100.0%; Score 414; DB 4; Length 414;
QY Best Local Similarity 100.0%; Pred. No. 0;
QY Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 MNPTLGIAIFLAVLITVKGILKSPSPRYKALSEVQKQKMAKELARQNDLGFKLL 60
QY 61 KKLAFNPGRNIFLSPISITAFSMLCIGADSTLDEIKQGFNFKMPEKDLHGFYIT 120
DB 61 KKLAFNPGRNIFLSPISITAFSMLCIGADSTLDEIKQGFNFKMPEKDLHGFYIT 120
QY 121 HELVKTODLKLSTIGNTLFDQRLQPKRFLKEDAKNYSATLITNFQNLMAOKOINDF 180

```

Db      121 HELTQTKDGLKLSIGNTLFLIDRLQPORKELEDAKNFYSAETLTITNFONLEMAQKQINDF 180
Qy      181 ISQKTHGKINNLINLEIDPGTVMLLANYIFPRARKHEFDNPVTKEEDPFLKNSSVKVPV 240
Db      181 ISQKTHGKINNLINLEIDPGTVMLLANYIFPRARKHEFDNPVTKEEDPFLKNSSVKVPV 240
Qy      241 MFRSGIYQVGYDVKLSTCTIIEIPYQKNITAFILPDGKIKHLKELQVDTFSRWKTLIS 300
Db      241 MFRSGIYQVGYDVKLSTCTIIEIPYQKNITAFILPDGKIKHLKELQVDTFSRWKTLIS 300
Qy      301 RRVAVDSVPRLLMTGTFDLKKTLISYGVSKIPEEHGDLTKIAPHRSLSKVGSAVHKAELKM 360
Db      301 RRVAVDSVPRLLMTGTFDLKKTLISYGVSKIPEEHGDLTKIAPHRSLSKVGSAVHKAELKM 360
Qy      361 DERGTGGAAGTGAQTLPMETPLVWKIDKPYLLIYSEKIPSVLFLGKIYNPIGK 414
Db      361 DERGTGGAAGTGAQTLPMETPLVWKIDKPYLLIYSEKIPSVLFLGKIYNPIGK 414

RESULT 2
AAE04885
ID      AAE04885 standard; protein; 414 AA.
XX
XX      AAE04885;
XX
XX      10-SEP-2001 (first entry)
XX
XX      Human protease protein-12 (PRTS-12).
XX
XX      Human; protease protein-12; PRTS-12; cytostatic; hypotensive; antiviral;
XX      gastrointestinal disorder; anorexia; dysphagia; cardiovascular disorder;
XX      atherosclerosis; vasculitis; autoimmune disorder; inflammatory disorder;
XX      Alzheimer's disease; cell proliferative disorder; dermatitis; cirrhosis;
XX      acquired immune deficiency syndrome; AIDS; neurological disorder; asthma;
XX      developmental disorder; epithelial disorder; eczema; dementia; noctropia;
XX      neurological disorder; reproductive disorder; infertility; teratogenesis;
XX      immunosuppressive; drug screening; actinic keratosis; cardiac; epilepsy;
XX      anaemia; antitumour; gene therapy; antibacterial.
XX
XX      Homo sapiens.
XX
XX      Key Peptide      Location/Qualifiers
XX      FT      1..19      /label= Signal_peptide
XX      FT      Protein      20..414
XX      FT      /note= "Mature human PRTS-12"
XX
XX      MO200146443-A2.
XX
XX      28-JUN-2001.
XX
XX      19-DEC-2000; 2000MO-US034811.
XX
XX      23-DEC-1999; 99US-0172055P.
XX      21-JAN-2000; 2000US-0177334P.
XX      28-JAN-2000; 2000US-0178884P.
XX      02-FEB-2000; 2000US-0179903P.
XX
XX      (INCY-) INCYTE GENOMICS INC.
XX
XX      Yang J, Baughn MR, Burford N, Au-Young J, Lu DM, Reddy R;
XX      Yue H, Nguyen DB, Tang YT, Yao MG, Lal P;
XX      WPI; 2001-418080/44.
XX      N-PSDB; AAD09549.
XX
XX      Novel human protease proteins (PRTS) useful for diagnosing, treating,
XX      preventing gastrointestinal, cardiovascular, autoimmune/inflammatory,
XX      cell proliferative disorders associated with abnormal expression of PRTS.
XX
XX      Claim 1, Page 118; 129pp; English.
XX
XX      The present sequence is human protease protein (PRTS-12). Human PRTS and

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CC      its nucleic acid molecule are useful for the diagnosis, treatment and
CC      prevention of disorders associated with increased or decreased expression
CC      of PRTS. Examples of such disorders include, gastrointestinal disorder
CC      such as anorexia, dysphagia; cardiovascular disorder such as
CC      atherosclerosis, vasculitis; autoimmune/inflammatory disorder such as
CC      acquired immune deficiency syndrome (AIDS), asthma; cell proliferative
CC      disorder such as actinic keratosis, cirrhosis; developmental disorder
CC      such as epilepsy, anaemia; epithelial disorder such as allergic contact
CC      dermatitis, eczema; neurological disorder such as Alzheimer's disease,
CC      dementia and reproductive disorder such as infertility and teratogenesis.
CC      PRTS DNA is useful for creating 'knockin' humanised animals (pigs) or
CC      transgenic animals (mice or rats) to model human disease. PRTS DNA is
CC      also in useful in gene therapy. PRTS and its immunogenic fragments are
CC      useful for screening libraries of compounds in several drug screening
CC      assays. PRTS is useful for analysing the proteome of a tissue or cell
CC      type
XX
XX      Sequence 414 AA;
XX
XX      Query Match      100.0%; Score 414; DB 4; Length 414;
XX      Best Local Similarity 100.0%; Pred. No. 0;
XX      Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy      1 MNPPTGLAIFLAVLLTVKGLKPSGSPNNYKALSEYQGMKQMAKELARQNMDLGFKLL 60
Db      1 MNPPTGLAIFLAVLLTVKGLKPSGSPNNYKALSEYQGMKQMAKELARQNMDLGFKLL 60
Qy      61 KGLAFNPGRNIFLPSLISIAFSMCLGADOSTDDEIQGFNFRMPKDLHEGFHYII 120
Db      61 KGLAFNPGRNIFLPSLISIAFSMCLGADOSTDDEIQGFNFRMPKDLHEGFHYII 120
Qy      121 HELTQTKDGLKLSIGNTLFLIDRLQPORKELEDAKNFYSAETLTITNFONLEMAQKQINDF 180
Db      121 HELTQTKDGLKLSIGNTLFLIDRLQPORKELEDAKNFYSAETLTITNFONLEMAQKQINDF 180
Qy      181 ISQKTHGKINNLINLEIDPGTVMLLANYIFPRARKHEFDNPVTKEEDPFLKNSSVKVPV 240
Db      181 ISQKTHGKINNLINLEIDPGTVMLLANYIFPRARKHEFDNPVTKEEDPFLKNSSVKVPV 240
Qy      241 MFRSGIYQVGYDVKLSTCTIIEIPYQKNITAFILPDGKIKHLKELQVDTFSRWKTLIS 300
Db      241 MFRSGIYQVGYDVKLSTCTIIEIPYQKNITAFILPDGKIKHLKELQVDTFSRWKTLIS 300
Qy      301 RRVAVDSVPRLLMTGTFDLKKTLISYGVSKIPEEHGDLTKIAPHRSLSKVGSAVHKAELKM 360
Db      301 RRVAVDSVPRLLMTGTFDLKKTLISYGVSKIPEEHGDLTKIAPHRSLSKVGSAVHKAELKM 360
Qy      361 DERGTGGAAGTGAQTLPMETPLVWKIDKPYLLIYSEKIPSVLFLGKIYNPIGK 414
Db      361 DERGTGGAAGTGAQTLPMETPLVWKIDKPYLLIYSEKIPSVLFLGKIYNPIGK 414

RESULT 3
ADA57300
ID      ADA57300 standard; protein; 414 AA.
XX
XX      ADA57300;
XX
XX      20-NOV-2003 (first entry)
XX
XX      Human secreted protein #583.
XX
XX      Immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
XX      cytostatic; cerebroprotective; neuroprotective; noctropic;
XX      cardiovascular; antiarteriosclerotic; gene therapy;
XX      human secreted protein; immune disorder; inflammation;
XX      respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
XX      inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
XX      multiple sclerosis; ischaemic brain injury; Parkinson's disease;
XX      Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
XX      triple helix formation; antisense gene therapy; forensic biology.
XX
XX      Homo sapiens.
XX

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XX W02002102994-A2.
 XX 27-DEC-2002.
 XX 19-MAR-2002; 2002WO-US008278.
 XX 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Ruben SM;
 PI WPI; 2003-167512/16.
 DR N-PSDB; ADA56404.
 XX
 PT New human secreted polypeptides and polynucleotides, useful for
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
 PT conditions, respiratory disorders, cancers, CNS disorders, or
 PT neurodegenerative disorders.
 PS Claim 13; SEQ ID NO 1490; 1754bp; English.
 XX
 CC The invention relates to 592 new human secreted polypeptides useful for
 CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
 CC conditions, respiratory disorders, cancers, CNS disorders, or
 CC neurodegenerative disorders, or polypeptides comprising an amino acid
 CC sequence at least 95% identical to the new sequences. The polypeptides,
 CC antibodies or antibody fragments that bind to the polypeptides, nucleic
 CC acids encoding the polypeptides, agonists or antagonists that binds to
 CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
 CC compositions for diagnosing, treating or preventing an e.g. immune
 CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
 CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
 CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
 CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
 CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
 CC polynucleotides are useful for chromosome identification, chromosome
 CC mapping, for controlling gene expression through triple helix formation
 CC or antisense DNA or RNA, in gene therapy, for identifying individuals
 CC from minute biological samples, in forensic biology, and as hybridization
 CC probes. The polypeptides are useful for as molecular weight markers on
 CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
 CC gels, to raise antibodies, for testing biological activities, and for
 CC treating or preventing neural disorders, immune system disorders,
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal, proliferative and/or cancerous diseases. This sequence corresponds
 CC to one of the polypeptide of the invention. Note: The sequence data for
 CC this patent did form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 414 AA;

Query Match 100.0%; Score 414; DB 6; Length 414;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTLGLAFLAVLTVKGLLKPSFSPRYKALSEVGMORMAKELARONMDLGPYKL 60
 DB 1 MNTTGLAIFLAVLTVKGLLKPSFSPRYKALSEVGMORMAKELARONMDLGPYKL 60
 QY 61 KKAFLNPGNNIFLSPISISTAFSMLCLGAQDSTLDEIKOGFNRKPKPEKOLHEGFYII 120
 DB 61 KKAFLNPGNNIFLSPISISTAFSMLCLGAQDSTLDEIKOGFNRKPKPEKOLHEGFYII 120
 QY 121 HELTOKTODKLSIGNTLFTIDORLQPKRKLEDAKNYSAFTIITNQNLEMAQKQINDP 180
 DB 121 HELTOKTODKLSIGNTLFTIDORLQPKRKLEDAKNYSAFTIITNQNLEMAQKQINDP 180

QY 181 ISQKHGKINNLINIDPGVMTLANIYIFPRAKWKHEPDVNTKGEDFLEKNSSVVKPM 240
 DB 181 ISQKHGKINNLINIDPGVMTLANIYIFPRAKWKHEPDVNTKGEDFLEKNSSVVKPM 240
 QY 241 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIPIIPDBGKLKHEKGLQVDTFSRWKTLIS 300
 DB 241 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIPIIPDBGKLKHEKGLQVDTFSRWKTLIS 300
 QY 301 RRVDVSVPRLMHTGTDLKKTLSYIGVSKIFEEHGLTKAPRSLKVGEAAVKAELKM 360
 DB 301 RRVDVSVPRLMHTGTDLKKTLSYIGVSKIFEEHGLTKAPRSLKVGEAAVKAELKM 360
 QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVFLGKIIVPIGK 414
 DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVFLGKIIVPIGK 414

RESULT 4
 ADA41179
 ID ADA41179 standard; protein; 414 AA.
 XX
 AC ADA41179;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted protein.

XX Human, secreted protein; cancer; hyperproliferative disorder;
 KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
 KW anaemia; allergic reaction; asthma; cardiovascular disorder;
 KW wound healing; cytotoxic; immunosuppressive; noctropic; neuroprotective;
 KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
 KW vulnereary; cardiant; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX W02002102993-A2.
 XX 27-DEC-2002.
 XX 19-MAR-2002; 2002WO-US008123.
 XX 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX Rosen CA, Ruben SM;
 PI WPI; 2003-175238/17.
 DR
 XX
 PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing,
 PT preventing or treating cancer or other hyperproliferative disorder,
 PT asthma, allergies or AIDS.
 PT
 PS Claim 1; SEQ ID NO 1561; 3205bp; English.
 PS

XX The invention relates to novel genes ADA39629-ADA40565 and proteins
 CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
 CC treating or ameliorating medical conditions e.g. by protein or gene
 CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
 CC fragments, and agonists or antagonists that bind to the polypeptide are
 CC useful for preparing a diagnostic or pharmaceutical composition for
 CC diagnosing or treating cancer or other hyperproliferative disorder. The
 CC polypeptides and nucleic acid molecules are also useful for detecting
 CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
 CC or other hyperproliferative disorders including neoplasms, autoimmune
 CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
 CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
 CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
 CC thrombocytopenia), allergic reactions including asthma or eczema,

CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
 CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
 CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
 CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
 CC fungal or viral infections including HIV/AIDS), or wound healing and
 CC disorders of epithelial cell proliferation. The nucleic acids are also
 CC useful for chromosome identification, radiation hybrid mapping or long-
 CC range restriction mapping, as molecular weight markers, or as
 CC hybridization or diagnostic probes. The polypeptides and antibodies are
 CC useful for providing immunological probes for differential identification
 CC of the tissues immunohistochemistry assays. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 414 AA;

Query Match 100.0%; Score 414; DB 6; Length 414;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;

Matches 414; Conservative 0; Indels 0; Gaps 0;

QY 1 MNPITGLAIFLAVLITVKGILKPSFSPRNKALSEVQGMKQMAAKELARQNMNDLGFKL 60
 DB 1 MNPITGLAIFLAVLITVKGILKPSFSPRNKALSEVQGMKQMAAKELARQNMNDLGFKL 60
 QY 61 KKLAFNPGRNIFLSPISISTAFSMCLGAQDSTLDEIKQFNFRKPEKDLHEGFHYII 120
 DB 61 KKLAFNPGRNIFLSPISISTAFSMCLGAQDSTLDEIKQFNFRKPEKDLHEGFHYII 120
 QY 121 HELTQKTQDLKLSIGNTLFTDRLQPKRFLDARKFSAETILTNFQMLEMAQKQINDF 180
 DB 121 HELTQKTQDLKLSIGNTLFTDRLQPKRFLDARKFSAETILTNFQMLEMAQKQINDF 180
 QY 181 ISOCTGKINLNIENIDPGTVMLANIYFFRARKHGFDPNTYKEEDFLEKNSSVKVP 240
 DB 181 ISOCTGKINLNIENIDPGTVMLANIYFFRARKHGFDPNTYKEEDFLEKNSSVKVP 240
 QY 241 MFRSGIYQGYDDKLSCTILIEIYQKNITAFILPDEGKLKHEKGLQVDTFSRWKTLIS 300
 DB 241 MFRSGIYQGYDDKLSCTILIEIYQKNITAFILPDEGKLKHEKGLQVDTFSRWKTLIS 300
 QY 301 RRVVDVSVRLMHTGTFDLKKTLSYIGVSKIPEBHGDLTKIAPHRSIKVGBAVHKAELKM 360
 DB 301 RRVVDVSVRLMHTGTFDLKKTLSYIGVSKIPEBHGDLTKIAPHRSIKVGBAVHKAELKM 360
 QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSYLFLGKIVNPIGK 414
 DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSYLFLGKIVNPIGK 414

RESULT 5

ADN05952
 ID ADN05952 standard; protein; 414 AA.

AC ADN05952;

DT 01-JUL-2004 (first entry)

DE Antipsoptic protein sequence #1136.

KM antipsoptic; gene therapy; psoriasis; diagnosis.

OS Homo sapiens.

PN WO2004028479-A2.

PD 08-APR-2004.

PF 25-SEP-2003; 2003WO-US030907.

PR 25-SEP-2002; 2002US-0414006P.

PA (GETH) GENENTECH INC.

XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WJ;
 PI Wu TD;
 XX WPI; 2004-305105/28.
 DR N-PSDB; ADN05951.

XX New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.

PS Claim 9; SEQ ID NO 2347; 3069pp; English.

CC The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.

CC Sequence 414 AA;

Query Match 100.0%; Score 414; DB 8; Length 414;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 414; Conservative 0; Indels 0; Gaps 0;

QY 1 MNPITGLAIFLAVLITVKGILKPSFSPRNKALSEVQGMKQMAAKELARQNMNDLGFKL 60
 DB 1 MNPITGLAIFLAVLITVKGILKPSFSPRNKALSEVQGMKQMAAKELARQNMNDLGFKL 60
 QY 61 KKLAFNPGRNIFLSPISISTAFSMCLGAQDSTLDEIKQFNFRKPEKDLHEGFHYII 120
 DB 61 KKLAFNPGRNIFLSPISISTAFSMCLGAQDSTLDEIKQFNFRKPEKDLHEGFHYII 120
 QY 121 HELTQKTQDLKLSIGNTLFTDRLQPKRFLDARKFSAETILTNFQMLEMAQKQINDF 180
 DB 121 HELTQKTQDLKLSIGNTLFTDRLQPKRFLDARKFSAETILTNFQMLEMAQKQINDF 180
 QY 181 ISOCTGKINLNIENIDPGTVMLANIYFFRARKHGFDPNTYKEEDFLEKNSSVKVP 240
 DB 181 ISOCTGKINLNIENIDPGTVMLANIYFFRARKHGFDPNTYKEEDFLEKNSSVKVP 240
 QY 241 MFRSGIYQGYDDKLSCTILIEIYQKNITAFILPDEGKLKHEKGLQVDTFSRWKTLIS 300
 DB 241 MFRSGIYQGYDDKLSCTILIEIYQKNITAFILPDEGKLKHEKGLQVDTFSRWKTLIS 300
 QY 301 RRVVDVSVRLMHTGTFDLKKTLSYIGVSKIPEBHGDLTKIAPHRSIKVGBAVHKAELKM 360
 DB 301 RRVVDVSVRLMHTGTFDLKKTLSYIGVSKIPEBHGDLTKIAPHRSIKVGBAVHKAELKM 360
 QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSYLFLGKIVNPIGK 414
 DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSYLFLGKIVNPIGK 414

RESULT 6

AA86217
 ID AA86217 standard; protein; 415 AA.

AC AA86217;

DT 19-APR-2000 (first entry)

DE Human secreted protein HWHGUS4, SEQ ID NO:132.

KM Human; secreted protein; cancer; tumour; developmental abnormality;
 KM foetal deficiency; blood disorder; immune system disorder; inflammation;
 KM autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 KM schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KM atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KM digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KM therapy.

OS Homo sapiens.

cell lines in biological samples and in antibody-based therapies for treating, inhibiting and preventing diseases, disorders or conditions associated with aberrant expression and/or activity of the above proteins. The antibody is useful for treating deficiencies or disorders of immune system and haematopoietic cells, for increasing differentiation and proliferation of haematopoietic cells, for treating immune deficiencies or disorders e.g. cancers, autoimmune disorders (such as rheumatoid arthritis and glomerulonephritis), HIV infection, anaemia and thrombocytopenia and as a marker for a particular immune system disease or disorder. The antibody is also useful for treating blood coagulation disorders, blood platelet disorders, wounds, heart attacks (infarction), strokes, scarring and asthma. The antibody is also useful for treating or preventing graft-versus host rejection, for modulating inflammation, for treating hyperproliferative disorders e.g. lymphoproliferative disorders and cancers, for inhibiting aberrant cellular division and for treating cell proliferative disorders. The antibody is also useful for treating cardiovascular disorders e.g. pulmonary heart disease and arrhythmia, disorders associated with neovascularization and angiogenesis, for treating hypertrophic scars and keloids, ocular disorders e.g. diabetic retinopathy and uveitis, for wound healing and disorders of epithelial cell proliferation. The antibody is also useful for treating neurological diseases e.g. Parkinson's disease, Alzheimer's disease, Huntington's chorea and amyotrophic lateral sclerosis (ALS), diseases associated with increased apoptosis e.g. AIDS, toxin induced liver disease, septic shock, cachexia and anorexia, for preventing and healing damage to lungs and for treating infectious diseases. The present sequence represents the amino acid sequence of a novel human secreted protein. Note: the sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docid=20030065151

Sequence 415 AA;

Query Match 100.0%; Score 414; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 NNPPTGLAIFLAVLLTVKGLKPSPPRYKALSEVQGMKMAKELARQNMDDGFKLL 60
DB 1 NNPPTGLAIFLAVLLTVKGLKPSPPRYKALSEVQGMKMAKELARQNMDDGFKLL 60
QY 61 KKLAFNPGRNIFLPLSISTAFSMLCIGAOSTLDEIKOGFNRKMPKEDLHEGPHYII 120
DB 61 KKLAFNPGRNIFLPLSISTAFSMLCIGAOSTLDEIKOGFNRKMPKEDLHEGPHYII 120
QY 121 HELTQKTODLKLKISGNTLFIIDQRLQPKRFLDANKFYSAETILTNFQULEMAQKINDF 180
DB 121 HELTQKTODLKLKISGNTLFIIDQRLQPKRFLDANKFYSAETILTNFQULEMAQKINDF 180
QY 122 HELTQKTODLKLKISGNTLFIIDQRLQPKRFLDANKFYSAETILTNFQULEMAQKINDF 180
DB 122 HELTQKTODLKLKISGNTLFIIDQRLQPKRFLDANKFYSAETILTNFQULEMAQKINDF 180
QY 181 ISQKTHGKINNLINENIDPGTVMLLANYIFFRARKGHEPDNVTKEEDFLEKNSVQVPM 240
DB 181 ISQKTHGKINNLINENIDPGTVMLLANYIFFRARKGHEPDNVTKEEDFLEKNSVQVPM 240
QY 241 MFRSGIYGVGYDQKSCITLFIYQKNITAFILPREGKLEKLEKLOVDPERRMTLLS 300
DB 241 MFRSGIYGVGYDQKSCITLFIYQKNITAFILPREGKLEKLEKLOVDPERRMTLLS 300
QY 301 RRVVDVSVRLHMTGTFDLKKTLSYIGVKIPEEHGDLTKIAPHRSILKYGEAVHKAELKM 360
DB 301 RRVVDVSVRLHMTGTFDLKKTLSYIGVKIPEEHGDLTKIAPHRSILKYGEAVHKAELKM 360
QY 361 DERGTGGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYNPIGK 414
DB 361 DERGTGGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKIYNPIGK 414

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RESULT 8

AAW78898 standard; protein; 414 AA.

AC AAW78898;

DT 06-NOV-2001 (first entry)

```

XX Human protein SEQ ID NO 1560.
DE
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KM tissue growth factor; immunomodulatory; cancer; leukaemia;
KM nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSB-) HYSBQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao Qa, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX MPI; 2001-476283/51.
XX
XX N-PSDB; AAKS2031.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.
XX
XX Claim 20; Page 3878-3879; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAKS1456-AAKS3435) and the
XX encoded polypeptides (AAW78823-AAW80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: Records for SEQ ID NO 2110 (AAKS2581), 2111
XX (AAKS2582) and 3666 (AAW80020) are omitted as the relevant pages from the
XX sequence listing were missing at the time of publication

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Sequence 414 AA;

Query Match 85.3%; Score 353; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 NNPPTGLAIFLAVLLTVKGLKPSPPRYKALSEVQGMKMAKELARQNMDDGFKLL 60
DB 1 NNPPTGLAIFLAVLLTVKGLKPSPPRYKALSEVQGMKMAKELARQNMDDGFKLL 60
QY 61 KKLAFNPGRNIFLPLSISTAFSMLCIGAOSTLDEIKOGFNRKMPKEDLHEGPHYII 120
DB 61 KKLAFNPGRNIFLPLSISTAFSMLCIGAOSTLDEIKOGFNRKMPKEDLHEGPHYII 120
QY 121 HELTQKTODLKLKISGNTLFIIDQRLQPKRFLDANKFYSAETILTNFQULEMAQKINDF 180
DB 121 HELTQKTODLKLKISGNTLFIIDQRLQPKRFLDANKFYSAETILTNFQULEMAQKINDF 180
QY 181 ISQKTHGKINNLINENIDPGTVMLLANYIFFRARKGHEPDNVTKEEDFLEKNSVQVPM 240
DB 181 ISQKTHGKINNLINENIDPGTVMLLANYIFFRARKGHEPDNVTKEEDFLEKNSVQVPM 240

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Db 181 ISQTHKINLNLENIDPGTVMLLANYIFFRARKHEDPNVTKEDPFLEKNSVAVPM 240
 QY MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIPIIPDEGKLKHEKGQVDFSRKTLIS 300
 CC |||||
 Db 241 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIPIIPDEGKLKHEKGQVDFSRKTLIS 300
 QY 301 RRVVDVSVPRHMTGTFDLTKTISYIGVSKIPEHGDLTAKAPHRSLKVGSAV 353
 Db 301 RRVVDVSVPRHMTGTFDLTKTISYIGVSKIPEHGDLTAKAPHRSLKVGSAV 353
 RESULT 9
 ID AAV05759 standard; protein; 358 AA.
 XX AAV05759;
 AC AAV05759;
 XX 24-OCT-2001 (first entry)
 DT Human NOV7 polypeptide #2.
 DE
 XX Human NOV7: A1J32990 B; fertility disorder; spermatogenesis; cardiant;
 KW cyrostatic; immunomodulatory; antiproliferative; antidiabetic;
 KW cell proliferation; cancer; diabetic retinopathy; angiogenic disorder;
 KW pulmonary disorder; haematopoietic disorder; immunological disorder;
 KW inflammatory disorder; tumour related disorders; emphysema; cirrhosis;
 KW wound healing; gene therapy.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 311..322
 FT /label= OTHER
 FT /note= "Other= Unknown"
 XX MO200149729-A2.
 XX 12-JUL-2001.
 PD 05-JAN-2001; 2001MO-US000299.
 PF 06-JAN-2000; 2000US-0174724P.
 PR 11-JAN-2000; 2000US-0175434P.
 PR 11-JAN-2000; 2000US-0175488P.
 PR 12-JAN-2000; 2000US-0175696P.
 PR 12-JAN-2000; 2000US-0175743P.
 PR 13-JAN-2000; 2000US-0175819P.
 PR 07-AUG-2000; 2000US-0223524P.
 PR 04-JAN-2001; 2001US-00755665.
 XX (CURA-) CURAGEN CORP.
 PA Prayaga SK, Majumder K, Tallon BE, Spaderna SK, Spytek KA,
 PI MacDougall J;
 XX WPI; 2001-418356/44.
 DR Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful
 XX for treating a syndrome associated with a NOVX-associated disorder, e.g.
 PT cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or
 PT pulmonary disorder.
 XX Disclosure; Page 33; 144pp; English.
 PS
 XX The invention relates to nucleic acids encoding NOVX (X being an integer
 CC from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
 CC useful in diagnosing, treating or manufacturing a medicament for a
 CC disease or disorder associated with NOVX e.g. cell proliferation (cancer
 CC and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
 CC disorders (e.g. of spermatogenesis), haematopoietic, immunological,
 CC inflammatory and tumour related disorders, emphysema, cirrhosis, wound
 CC healing. NOVX nucleic acids are also useful in gene therapy. They are
 CC also used for screening for a modulator of activity or of latency or

CC predisposition to a NOVX-associated disorder. They are also useful for
 CC determining the presence of or predisposition to a NOVX-associated
 CC disorder. The present sequence represents a version of NOV7 (A1J32990 B)
 CC appearing in table 25 of the specification, which has sequence homology
 CC to an unidentified human secreted protein (HMGUS54) and to alpha anti-
 CC trypsin
 XX
 SQ Sequence 358 AA;
 Query Match 74.9%; Score 310; DB 4; Length 358;
 Best Local Similarity 100.0%; Pred. No. 4.1e-294;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 54 DLGFKLKCLAFNPGNITLSPISISTAFSMTCLGAQDSTLDBIKQFNFRKPEKDLH 113
 Db 1 DLGFKLKCLAFNPGNITLSPISISTAFSMTCLGAQDSTLDBIKQFNFRKPEKDLH 60
 QY 114 EGFHYIIHETLTKTODKLSIGNTLFDQLQPKRKTLEDKKNFYSAETLLTNFQLEMA 173
 Db 61 EGFHYIIHETLTKTODKLSIGNTLFDQLQPKRKTLEDKKNFYSAETLLTNFQLEMA 120
 QY 174 QKQINDPISQKTKGKINLNLENIDPGTVMLLANYIFFRARKHEDPNVTKEDPFLEKN 233
 Db 121 QKQINDPISQKTKGKINLNLENIDPGTVMLLANYIFFRARKHEDPNVTKEDPFLEKN 180
 QY 234 SSYKVPMMFRSGIYQVGYDDKLSCTTILEIPYQKNITAIPIIPDEGKLKHEKGQVDFSR 293
 Db 181 SSYKVPMMFRSGIYQVGYDDKLSCTTILEIPYQKNITAIPIIPDEGKLKHEKGQVDFSR 240
 QY 294 RKMTLLSRVVDVSVPRHMTGTFDLTKTISYIGVSKIPEHGDLTAKAPHRSLKVGSAV 353
 Db 241 RKMTLLSRVVDVSVPRHMTGTFDLTKTISYIGVSKIPEHGDLTAKAPHRSLKVGSAV 300
 QY 354 HKAKLKXDER 363
 Db 301 HKAKLKXDER 310
 RESULT 10
 ID ABB11832 standard; peptide; 431 AA.
 XX ABB11832;
 AC ABB11832;
 DT 11-JAN-2002 (first entry)
 DE Human secreted protein homologue, SEQ ID NO:2202.
 DS
 XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antisthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cyrostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antitumor.
 XX Homo sapiens.
 OS
 XX WO200157188-A2.
 XX 09-AUG-2001.
 PD 05-FEB-2001; 2001MO-US003800.
 PF 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX

PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI: 2001-457740/49.
 DR N-PSDB, ABA09076.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 PS Claim 20; Page 263; 1963pp; English.
 XX
 CC Sequences ABA10981-ABA12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoietic regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention
 CC
 XX
 SQ Sequence 431 AA;
 Query Match 43.7%; Score 181; DB 4; Length 431;
 Best Local Similarity 100.0%; Pred. No. 7e-168;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NMPTGLAIFLAVLITVVGKLPSPSPRYKALSEVQGMKORMAKELARQNMDDGFKLL 60
 Db NMPTGLAIFLAVLITVVGKLPSPSPRYKALSEVQGMKORMAKELARQNMDDGFKLL 77
 Oy 61 KKLAFYNGRNIPLSPISISTAFSMLCLGAQDSTLDEIKQGFNRKMPKDLHEGFHYII 120
 Db KKLAFYNGRNIPLSPISISTAFSMLCLGAQDSTLDEIKQGFNRKMPKDLHEGFHYII 137
 Oy 78 KKLAFYNGRNIPLSPISISTAFSMLCLGAQDSTLDEIKQGFNRKMPKDLHEGFHYII 137
 Db 121 HELTQKTDKLKLSIGNTLTIDQRLQQRKFLBDKAKFYSAETLLTNFQMLEMAQKINDP 180
 138 HELTQKTDKLKLSIGNTLTIDQRLQQRKFLBDKAKFYSAETLLTNFQMLEMAQKINDP 197
 Oy 181 I 181
 Db 198 I 198

RESULT 11
 AAM79882
 ID AAM79882 standard; protein; 431 AA.
 XX
 AC AAM79882;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 3528.
 XX
 KM Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KM tissue growth factor; immunomodulatory; cancer; leukaemia;
 KM nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200157190-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001WO-US004098.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654935.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Gao Y;
 PI Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 DR WPI: 2001-476283/51.
 DR N-PSDB; AAK53015.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 XX
 PS Claim 20; Page 371; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM76323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoietic regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52881), 2111
 CC (AAK52882) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 CC
 XX
 SQ Sequence 431 AA;
 Query Match 43.7%; Score 181; DB 4; Length 431;
 Best Local Similarity 100.0%; Pred. No. 7e-168;
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 NMPTGLAIFLAVLITVVGKLPSPSPRYKALSEVQGMKORMAKELARQNMDDGFKLL 60
 Db NMPTGLAIFLAVLITVVGKLPSPSPRYKALSEVQGMKORMAKELARQNMDDGFKLL 77
 Oy 61 KKLAFYNGRNIPLSPISISTAFSMLCLGAQDSTLDEIKQGFNRKMPKDLHEGFHYII 120
 181 I 181
 Db 198 I 198

Db 78 KGLAFYNGRNIFLSPISISTAFSMLCLGADSTLDEIKOGFNPKPEKDLHEGFHYII 137
 QY 121 HELTQKTQDLKLSIGNTLFIPIORLQPKFLEDAKNFYSAETITLNFONLEMAKQINDF 180
 Db 138 HELTQKTQDLKLSIGNTLFIPIORLQPKFLEDAKNFYSAETITLNFONLEMAKQINDF 197
 QY 181 I 181
 Db 198 I 198

RESULT 12

AAM70426
 ID AAM70426 standard; protein; 140 AA.

AC AAM70426;
 XX

DT 06-NOV-2001 (first entry)
 XX

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 30732.
 XX

KM Human; bone marrow expressed exon; gene expression analysis; probe;
 KM microarray; cancer; leukaemia; lymphoma; myeloma.
 OS Homo sapiens.

PN WO200157276-A2.
 XX

PD 09-AUG-2001.
 XX

PF 30-JAN-2001; 2001WO-US000668.
 XX

PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.
 XX

PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX

DR WPI; 2001-488900/53.
 XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 XX

PS Example 4; SEQ ID NO 30732; 658bp + Sequence Listing; English.
 XX

CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention
 XX

SQ Sequence 140 AA;
 XX

Query Match 31.2%; Score 129; DB 4; Length 140;
 Best Local Similarity 100.0%; Pred. No. 2e-117;

Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 FSWLCLGAGDSTLDEIKOGFNPKPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIPIQ 142
 Db 1 FSWLCLGAGDSTLDEIKOGFNPKPEKDLHEGFHYIIHELTQKTQDLKLSIGNTLFIPIQ 60

QY 143 RLQPKRFLLEDANKFYSAETITLNFONLEMAKQINDFISOKTHGKTNLLENIDPGTVM 202
 Db 61 RLQPKRFLLEDANKFYSAETITLNFONLEMAKQINDFISOKTHGKTNLLENIDPGTVM 120

QY 203 LLANYIFFR 211

Db 121 LLANYIFFR 129

Search completed: March 31, 2006, 10:02:29
 Job time : 224.573 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 31, 2006, 10:02:58 ; Search time 26.0989 Seconds
(without alignments)
1526.262 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 414
Sequence: 1 MNPTLGAIPIAVLITVKGL.....YSEKIPSVLFGKIVNPICK 414

Scoring matrix: BLO62
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 15
Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : PIR_80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
No matches found				

Search completed: March 31, 2006, 10:08:39
Job time : 26.0989 secs

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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 31, 2006, 09:55:21 ; Search time 157.105 Seconds
(without alignments)
1859.193 Million cell updates/sec

Title: US-10-664-356-1562

Perfect score: 414
Sequence: 1 MNPTGLAIFLAVALTVKGL.....YSEKIPSVLFGKIVNPFGK 414

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size: 15

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database: UniProt_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB	ID
1	414	100.0	414	2 Q81W75 HUMAN
2	19	4.6	413	2 Q7TWF5 MOUSE
3	19	4.6	413	2 O9CQ32 MOUSE
4	19	4.6	413	2 O6P6M3 MOUSE
5	16	3.9	411	2 Q8R4Z1 RAT

ALIGNMENTS

RESULT 1
Q81W75 HUMAN
ID Q81W75_HUMAN PRELIMINARY; PRT; 414 AA.
AC Q81W75;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Serine (Or cysteine) proteinase inhibitor, clade A (Alpha-1
antitrypsinase, antitrypsin), member 12 (Ol-64) (Visceral adipose-
specific SERPIN).
GN Name=SERPIN12;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Homo.
OX NCBI_TaxID=9606;
RN NCULEOTIDE SEQUENCE.
RP TISSUE=Skin;
RC MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stampleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carrincci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywnicki M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.W., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences." J.
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NCULEOTIDE SEQUENCE.
RC TISSUE=Skin;
RG NIH WGC Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NCULEOTIDE SEQUENCE.
RC TISSUE=Heart;
RG Chen S., Guo J.H., Yu L.,
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NCULEOTIDE SEQUENCE.
RA Hida K., Wada J., Zhang H.,
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL; BC040857; AA040857.1; -; mRNA.
DR EMBL; AY177692; AA018649.1; -; mRNA.
DR HSSP; P01009; 10MB.
DR Ensembl; ENSG00000165953; Homo sapiens.
DR HGNC; HGNC:18359; SERPINA12.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
KW Serpin.
SQ SEQUENCE 414 AA; 47175 MW; 5C70F1AB5935661C CRC64;
Query Match 100.0%; Score 414; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNPTGLAIFLAVALTVKGLKPSFSPRYKALSEVQGMQRMAKELARQNDLGFRL 60
DB 1 MNPTGLAIFLAVALTVKGLKPSFSPRYKALSEVQGMQRMAKELARQNDLGFRL 60
QY 61 KCLAFVNGRNIFLSPISSTAFSMLCLGAODSTLDEIKGFNRKRPEDLHGFYII 120
DB 61 KCLAFVNGRNIFLSPISSTAFSMLCLGAODSTLDEIKGFNRKRPEDLHGFYII 120
QY 121 HELTQKTDKLKLSIGNTLFDORLQPORKELEDAKNFSAETILTNFQNTLMAQKQINDF 180
DB 121 HELTQKTDKLKLSIGNTLFDORLQPORKELEDAKNFSAETILTNFQNTLMAQKQINDF 180
QY 181 ISQKTHGKINLLENIDPGTVMLLANYIFFRARWKHEFDNVTKEDPFLKSSVAVPM 240
DB 181 ISQKTHGKINLLENIDPGTVMLLANYIFFRARWKHEFDNVTKEDPFLKSSVAVPM 240
QY 241 MPRSGIYGVGDKLSCCTIIEIPYOKNITAIFLTPBGKXKHEKGQVTPSRMKLLS 300
DB 241 MPRSGIYGVGDKLSCCTIIEIPYOKNITAIFLTPBGKXKHEKGQVTPSRMKLLS 300
QY 301 RRVVDVSVPLHNTGTFDLKLTSLYIGVSKIFPEHGDLTKIADPRSLKVGAAVHKELKM 360
DB 301 RRVVDVSVPLHNTGTFDLKLTSLYIGVSKIFPEHGDLTKIADPRSLKVGAAVHKELKM 360

DB 301 RRVVDVSPRLHMTGTREDLTKLTISYIGSVKIPFEHGDLTAKIAPRSLKGVBAVHAKELKM 360

QY 361 DERGTGAGAGAGACTPLMETPLVYKIDKPYLLIYSEKIPSVLPLGIYNVPIGK 414

DB 361 DERGTGAGAGAGACTPLMETPLVYKIDKPYLLIYSEKIPSVLPLGIYNVPIGK 414

RESULT 2

Q7TWF5_MOUSE PRELIMINARY; PRT; 413 AA.

AC 01-OCT-2003 (TREMBlrel. 25, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)

DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Visceral adipose-specific SERPIN.

GN Name=Serpin12;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Swiss Webster;

RA Hida K., Wada J., Zhang H.;

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the serpin family.

DR EMBL: AY326419; AAP88363.1; -; mRNA.

DR HSSP: P01008; 1ATH.

DR MGI: MGI:1915304; Serpin12.

DR GO: GO:0005615; C:extracellular space; TAS.

DR InterPro: IPR000295; Prot_inh_Lesrp2.

DR InterPro: IPR000215; Prot_inh_serpin.

DR Pfam: PF00079; Serpin; 1.

DR PRINTS: PR00780; LEUSERPINII.

DR SMART: SM00093; SERPIN; 1.

DR PROSITE: PS00284; SERPIN; 1.

KW Serpin.

SQ SEQUENCE 413 AA; 47674 MW; EE2B3B08C2DD418F CRC64;

Query Match 4.6%; Score 19; DB 2; Length 413;

Best Local Similarity 100.0%; Pred. No. 4.5e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 344 HRLKLVGEAVHAKELKXDE 362

DB 344 HRLKLVGEAVHAKELKXDE 362

RESULT 3

Q9CQ32_MOUSE PRELIMINARY; PRT; 413 AA.

AC 09CQ32;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE 01-FEB-2005 (TREMBlrel. 29, Last annotation update)

DE Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632419J12 product:hypothetical Serpins containing protein, full insert sequence (Mus musculus 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3300001F13 product:hypothetical Serpins containing protein, full insert sequence).

GN Name=Serpin12;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Mech. Enzymol. 303:19-44(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schirml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofman M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Maehima Y., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,

RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohenki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;

RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,

RA Nikaide I., Oosato N., Saito R., Suzuki H., Yamataka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,

RA Balderelli R., Hill D.P., Bull C., Hume D.A., Quackenbush J.,

RA Schirml L.M., Kanpin A., Matsuda H., Batalov S., Beisel K.W.,

RA Blake J.A., Brad D., Brusic V., Chotina C., Coban L.B., Konstant S.,

RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,

RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson J.J., Jarvis E.D.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maglocz D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Sempie C.A., Seton M., Shimada M.,

RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Verardo R., Wagner L., Walestedt C., Wang Y., Watanabe Y., Wells C.,

RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,

RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,

RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [4]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,

RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subcloning of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

RN [5]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;

RX MEDLINE=20350913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

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RA Komno H., Akiyama J., Nishi K., Kitsuai T., Teshiro H., Itoh M.,
RA Sunit N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa K., Ozawa K., Tanaka T., Matsura S., Kanai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multiplexed sequencing."
RL Genome Res. 10:1757-1771(2000).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Komno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamori T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL; AK014589; BAB29447.1; -; mRNA.
DR EMBL; AK014346; BAB29287.1; -; mRNA.
DR HSSP; P01008; IATH.
DR Ensemble; ENSMUSG00000041567; Mus musculus.
DR MGI; MGI:1915304; Serpina12.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000295; Prot_inh_lseerp2.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR PRINTS; PR00780; LEUSERPINIT.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
DR Hypothetical protein; Serpin.
DR KW SEQUENCE 413 AA; 47634 MW; DOAB8E1BE24FD60A CRC64;

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Best Local Similarity 100.0%; Pred. No. 4.5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 344 HRSIKVGEAVHAKELKXDE 362

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AC Q6PEM3_MOUSE PRELIMINARY; PRT; 413 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Visceral adipose-specific SERPIN.
GN Name=Serpina12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Jaw and Limb;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatczenko L., Marulita K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bosa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Raik S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunatratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
RA Scherich A., Schein J.E., Jones S.J.M., Maiz A.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Jaw and Limb;
RG NIH WGC Project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL; BC062143; AAH62143.1; -; mRNA.
DR HSSP; P01008; IATH.
DR Ensemble; ENSMUSG00000041567; Mus musculus.
DR MGI; MGI:1915304; Serpina12.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000295; Prot_inh_lseerp2.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR PRINTS; PR00780; LEUSERPINIT.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; UNKNOWN_1.
DR KW SEQUENCE 413 AA; 47630 MW; CE1940BA2EBE5811 CRC64;

Query Match 4.6%; Score 19; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 4.5e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 344 HRSIKVGEAVHAKELKXDE 362
Db 344 HRSIKVGEAVHAKELKXDE 362

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ID Q6R4Z1_RAT PRELIMINARY; PRT; 411 AA.
AC Q6R4Z1_RAT PRELIMINARY; PRT; 411 AA.
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Visceral adipose tissue specific SERPIN.
GN Name=Serpina12; Synonym=Vaspin;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OLETF; TISSUE=Visceral adipose;
RA Hida K., Wada J., Zhang H., Shikata K., Makino H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL; AF245398; AAU9574.1; -; mRNA.
DR HSSP; P01008; IATH.
DR Ensemble; ENSRNOG00000009710; Rattus norvegicus.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000295; Prot_inh_lseerp2.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR PRINTS; PR00780; LEUSERPINIT.
DR SMART; SM00093; SERPIN; 1.

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KW Serpin. 411 AA; 47527 MW; 29FA271FF8CC8A2D CRC64;
SQ SEQUENCE

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Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 71 NIFLSPUSISTAFSML 86

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Job time : 159.105 secs

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OM protein - protein search, using SW model

Run on: March 31, 2006, 10:08:07 ; Search time 33.775 Seconds
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Gapop 60.0 , Gapext 60.0

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Word size: 35

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SUMMARIES

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1	414	100.0	414	2	US-09-755-665-14 Sequence 14, Appl
2	414	100.0	414	2	US-09-755-665-55 Sequence 55, Appl
3	414	100.0	414	2	US-09-755-665-56 Sequence 56, Appl
4	414	100.0	415	2	US-09-461-325-134 Sequence 134, App
5	414	100.0	415	2	US-10-012-542-134 Sequence 134, App
6	414	100.0	415	2	US-10-115-123-134 Sequence 134, App
7	310	74.9	361	2	US-09-755-665-57 Sequence 57, Appl

ALIGNMENTS

RESULT 1
US-09-755-665-14
; Sequence 14, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailion, Bruce E.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14

; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-14

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 KCLAFVNGRNIFLSPISLSTAFSMLCLGAQDSTLDEIKOGFNRKPEKDLHEGFYII 120
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DB 121 HELTOKTODIKLSIGNTLFTIDRLQPKRFLDPAKNFSAETITNFQNTLEMAQKQINDF 180
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DB 181 ISOKTGKINNLLENIDPGTVMILANYIFPRARKHEFDNNTKEEDFLEKSSVAVPM 240
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DB 241 MPFSGIYQVGYDDKLSCTTIEIPYQKNITAFILPDEGKLKHEKGLQVTFPSRKTLIS 300
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DB 361 DERGTGAAGTGAQOTLPMETPLVVKIDPYLLIYSEKIPSVLFGKIVNPIGK 414

RESULT 2
US-09-755-665-55
; Sequence 55, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailion, Bruce E.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 55
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-55

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 RRVDVSVRLMHTGTFDLKTLSTYIGVSKIPEHGDLTKLAPHRSIKVGEAVHKAELKM 360
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RESULT 3

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US-09-755-665-56
; Sequence 56, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailom, Bruce E.
; APPLICANT: Spaderma, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755, 665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-56
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 KKLAFYNGRNIFLSPPLSTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHGFHYII 120
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RESULT 4

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US-09-461-325-134
; Sequence 134, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
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; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-09-461-325-134
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Query Match 100.0%; Score 414; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 KKLAFYNGRNIFLSPPLSTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHGFHYII 120
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Db 121 HELTQTDKLKLSIGNTLFIIDQRLQPKFLEDAKQFSAETILLNPNQLEMAQKQINDF 180
Qy 181 ISQKTHGKINNLIENIDPGTWMLANIYIFFRARWKEHFDPNVTKEDDFLEKSSSVKVP 240
Db 181 ISQKTHGKINNLIENIDPGTWMLANIYIFFRARWKEHFDPNVTKEDDFLEKSSSVKVP 240
Qy 241 MFRSGIYGVYDDKLSCTILFIYQKNITAFILPDEGKLKLEKGLQVDTFSRMKTLIS 300
Db 241 MFRSGIYGVYDDKLSCTILFIYQKNITAFILPDEGKLKLEKGLQVDTFSRMKTLIS 300
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Qy 301 RRVVDVSVPLHMTGTEDLKKTLISYIGVSKI FEEHGDLTAKIAPRSLKVGSAVHAKELKM 360
Db 301 RRVVDVSVPLHMTGTEDLKKTLISYIGVSKI FEEHGDLTAKIAPRSLKVGSAVHAKELKM 360
Qy 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKI VPIGK 414
Db 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKI VPIGK 414

RESULT 5

US-10-012-542-134
; Sequence 134, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino
; OTHER INFORMATION: acids
US-10-012-542-134

Query Match 100.0%; Score 414; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MNPTGLAIFLAVALTVKGLLKPSFSPRNYKALSEVGWQRMARAKELARQNDLGFRL 60
Qy 61 KKAAPYNGNITPLSPISISTAFSMLCLGAQDSTLDEIKOGFNRKRPKPEKOLHGFHYII 120
Db 61 KKAAPYNGNITPLSPISISTAFSMLCLGAQDSTLDEIKOGFNRKRPKPEKOLHGFHYII 120
Qy 121 HELTQKTQDLKLSIGNTLFLDQRLQPKRFLBDKAKNYSATLITNFQNLMAQKQINDF 180
Db 121 HELTQKTQDLKLSIGNTLFLDQRLQPKRFLBDKAKNYSATLITNFQNLMAQKQINDF 180
Qy 121 ISQTHGKINNLIENIDPGTVMLLANYIFPRARWKHEFDPNVTKBEDFLEKNSSVKVP 240
Db 121 ISQTHGKINNLIENIDPGTVMLLANYIFPRARWKHEFDPNVTKBEDFLEKNSSVKVP 240
Qy 181 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIPLPDEGKLKHEKGLQVDTFSRWKTLIS 300
Db 181 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIPLPDEGKLKHEKGLQVDTFSRWKTLIS 300
Qy 241 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIPLPDEGKLKHEKGLQVDTFSRWKTLIS 300
Db 241 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIPLPDEGKLKHEKGLQVDTFSRWKTLIS 300
Qy 301 RRVVDVSVPLHMTGTEDLKKTLISYIGVSKI FEEHGDLTAKIAPRSLKVGSAVHAKELKM 360
Db 301 RRVVDVSVPLHMTGTEDLKKTLISYIGVSKI FEEHGDLTAKIAPRSLKVGSAVHAKELKM 360

Qy 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKI VPIGK 414
Db 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKI VPIGK 414

RESULT 6

US-10-115-123-134
; Sequence 134, Application US/10115123
; Patent No. 674216
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029G30AP1D2
; CURRENT APPLICATION NUMBER: US/10/115,123
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-115-123-134

Query Match 100.0%; Score 414; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNPTGLAIFLAVALTVKGLLKPSFSPRNYKALSEVGWQRMARAKELARQNDLGFRL 60
Db 1 MNPTGLAIFLAVALTVKGLLKPSFSPRNYKALSEVGWQRMARAKELARQNDLGFRL 60
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Db 61 KKAAPYNGNITPLSPISISTAFSMLCLGAQDSTLDEIKOGFNRKRPKPEKOLHGFHYII 120
Qy 121 HELTQKTQDLKLSIGNTLFLDQRLQPKRFLBDKAKNYSATLITNFQNLMAQKQINDF 180
Db 121 HELTQKTQDLKLSIGNTLFLDQRLQPKRFLBDKAKNYSATLITNFQNLMAQKQINDF 180
Qy 121 ISQTHGKINNLIENIDPGTVMLLANYIFPRARWKHEFDPNVTKBEDFLEKNSSVKVP 240
Db 121 ISQTHGKINNLIENIDPGTVMLLANYIFPRARWKHEFDPNVTKBEDFLEKNSSVKVP 240
Qy 181 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIPLPDEGKLKHEKGLQVDTFSRWKTLIS 300
Db 181 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIPLPDEGKLKHEKGLQVDTFSRWKTLIS 300
Qy 241 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIPLPDEGKLKHEKGLQVDTFSRWKTLIS 300
Db 241 MFRSGIYQVGYDDKLSCTTILEIPYQKNITAIPLPDEGKLKHEKGLQVDTFSRWKTLIS 300
Qy 301 RRVVDVSVPLHMTGTEDLKKTLISYIGVSKI FEEHGDLTAKIAPRSLKVGSAVHAKELKM 360
Db 301 RRVVDVSVPLHMTGTEDLKKTLISYIGVSKI FEEHGDLTAKIAPRSLKVGSAVHAKELKM 360
Qy 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKI VPIGK 414
Db 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGKI VPIGK 414

RESULT 7
US-09-755-665-57
Sequence 57, Application US/09755665
Patent No. 6600019
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tailon, Bruce B.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
LENGTH: 361
TYPER: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)..(361)
OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
OTHER INFORMATION: specification
US-09-755-665-57

Send data

Query Match 74.9%; Score 310; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 2.3e-292;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 54 DLGFKLLKLAFFNPGNIFLPLSLSTAFSMLCLGAQDSTLDEIKGFNFRMPKDLH 113
DB 1 DLGFKLLKLAFFNPGNIFLPLSLSTAFSMLCLGAQDSTLDEIKGFNFRMPKDLH 60
QY 114 EGFHYIHELTQTDLKLSTIGNTLFLDRLQPKRFLBDKKNFYSARTILTNFQNLKMA 173
DB 61 EGFHYIHELTQTDLKLSTIGNTLFLDRLQPKRFLBDKKNFYSARTILTNFQNLKMA 120
QY 174 OKQINDFISQKTHGKINLNIENIDPGTVMLANIIFPRAMKHEPDPNVTKEEDFFLEKX 233
DB 121 OKQINDFISQKTHGKINLNIENIDPGTVMLANIIFPRAMKHEPDPNVTKEEDFFLEKX 180
QY 234 SSVKVPMMFRSGIYQVGYDDKLSCTTLEIPYQKNITAIPLPDEGKLKHEKGLQVDTFS 293
DB 181 SSVKVPMMFRSGIYQVGYDDKLSCTTLEIPYQKNITAIPLPDEGKLKHEKGLQVDTFS 240
QY 294 RMKTTLSRRVVDVSVRLHMTGTFDLKKTLSYGVSKIPREHGLTKIAPHRSIKVGEAV 353
DB 241 RMKTTLSRRVVDVSVRLHMTGTFDLKKTLSYGVSKIPREHGLTKIAPHRSIKVGEAV 300
QY 354 HKAEIKMDER 363
DB 301 HKAEIKMDER 310

Search completed: March 31, 2006, 10:09:51
Job time : 33.775 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 31, 2006, 10:08:54 ; Search time 120.26 Seconds
(without alignments)
1438.400 Million cell updates/sec

Title: US-10-664-356-1562
Perfect score: 414
Sequence: 1 MNPTLGAIPLAVLITVKGK.....YSEKIPSVLFGKIVNPICK 414

*Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size: 15

Total number of hits satisfying chosen parameters: 14

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database: Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	414	100.0	414	3	US-09-755-665-14 Sequence 14, App1
2	414	100.0	414	3	US-09-755-665-55 Sequence 55, App1
3	414	100.0	414	3	US-09-755-665-56 Sequence 56, App1
4	414	100.0	414	4	US-10-168-425-12 Sequence 12, App1
5	414	100.0	414	4	US-10-629-248-14 Sequence 14, App1
6	414	100.0	414	4	US-10-629-248-55 Sequence 55, App1
7	414	100.0	414	4	US-10-629-248-56 Sequence 56, App1
8	414	100.0	414	4	US-10-012-542-134 Sequence 134, App1
9	414	100.0	414	4	US-10-115-123-134 Sequence 115, App1
10	414	100.0	414	4	US-10-800-834-134 Sequence 134, App1
11	310	74.9	361	3	US-09-755-665-57 Sequence 57, App1
12	310	74.9	361	4	US-10-629-248-57 Sequence 57, App1
13	181	43.7	431	4	US-10-276-774-2202 Sequence 2202, App1
14	129	31.2	140	3	US-09-864-761-48438 Sequence 48438, App1

ALIGNMENTS

RESULT 1
US-09-755-665-14 Application US/09755665
; Sequence 14, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce E.

APPLICANT: Spaderna, Steven K.
APPLICANT: Spylek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-09-755-665-14

Query Match 100.0%; Score 414; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNPTLGAIPLAVLITVKGKLSFSPRNKALSEVQGMKQMAKELARQNDLGFKL	60
DB	1	MNPTLGAIPLAVLITVKGKLSFSPRNKALSEVQGMKQMAKELARQNDLGFKL	60
QY	61	KGLAFVNGRNTFSPLSISTAFSMLCIGAQDSTLDEIKQGFNRKMEKDLHGPHYII	120
DB	61	KGLAFVNGRNTFSPLSISTAFSMLCIGAQDSTLDEIKQGFNRKMEKDLHGPHYII	120
QY	121	HELTQKQDQKLSIGNTLFDQRLQPKELADAKNFSAETLLTNFQNLMAQKQINDF	180
DB	121	HELTQKQDQKLSIGNTLFDQRLQPKELADAKNFSAETLLTNFQNLMAQKQINDF	180
QY	181	ISQTKGKINLLENIDPQTMLLANYIFPRARKHEFDNVTKEEDFLEKSSVQVPM	240
DB	181	ISQTKGKINLLENIDPQTMLLANYIFPRARKHEFDNVTKEEDFLEKSSVQVPM	240
QY	241	MPSGTYQVGYDQKLSCTILEIPYQKNITAFILPBGKIKHLEKQVDFPSRWKTLIS	300
DB	241	MPSGTYQVGYDQKLSCTILEIPYQKNITAFILPBGKIKHLEKQVDFPSRWKTLIS	300
QY	301	RRVVDVSVPRILHNTGTFDLKKTLSYIGSVKIFEEHGDLTICADPRSLKVGSAVHKELKM	360
DB	301	RRVVDVSVPRILHNTGTFDLKKTLSYIGSVKIFEEHGDLTICADPRSLKVGSAVHKELKM	360
QY	361	DERGTGAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVFLGKIVNPICK	414
DB	361	DERGTGAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVFLGKIVNPICK	414

RESULT 2
US-09-755-665-55
; Sequence 55, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spylek, Kimberly A.
; APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens

US-09-755-665-55

Query Match 100.0%; Score 414; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MNPTGLAIPLAVILTVYKGLKPSFSPRNKALSEVQGMKORMAKELARQNDLGFKLL 60
QY 61 KKLAFNPGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHGFHYII 120
DB 61 KKLAFNPGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHGFHYII 120
QY 121 HELTOKTQDLKLSIGNTLFIIDQRLQPORKFLEDAKNFYSAETILTNFQNLMAQKQINDF 180
DB 121 HELTOKTQDLKLSIGNTLFIIDQRLQPORKFLEDAKNFYSAETILTNFQNLMAQKQINDF 180
QY 181 ISOCTHGKINNLINENIDPGTVMLANIYIFPRARWKHEFDPNVTKEEDFLEKNSSVKVP 240
DB 181 ISOCTHGKINNLINENIDPGTVMLANIYIFPRARWKHEFDPNVTKEEDFLEKNSSVKVP 240
QY 241 MFRSGIYQVGYDDKLSCTTILFIYQKNITAIPIIPDEGKLNLEKGLQVDFSRMKTLLS 300
DB 241 MFRSGIYQVGYDDKLSCTTILFIYQKNITAIPIIPDEGKLNLEKGLQVDFSRMKTLLS 300
QY 301 RRVVDVSVPLNHTGTFDCLKTSLYIGVSKIPIEBHGLTKIAPHRSIKVGEAVHAKELKM 360
DB 301 RRVVDVSVPLNHTGTFDCLKTSLYIGVSKIPIEBHGLTKIAPHRSIKVGEAVHAKELKM 360
QY 361 DERGTGAAGTGAGTLPMEETPLVVKIDKPYLLIYSBKIPSVLFLKIVNPICK 414
DB 361 DERGTGAAGTGAGTLPMEETPLVVKIDKPYLLIYSBKIPSVLFLKIVNPICK 414

RESULT 3

US-09-755-665-56
Sequence 56; Application US/09755665
Patent No. US20020107186A1
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tallion, Bruce E.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 56
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-09-755-665-56

Query Match 100.0%; Score 414; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIPLAVILTVYKGLKPSFSPRNKALSEVQGMKORMAKELARQNDLGFKLL 60
DB 1 MNPTGLAIPLAVILTVYKGLKPSFSPRNKALSEVQGMKORMAKELARQNDLGFKLL 60
QY 61 KKLAFNPGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHGFHYII 120
DB 61 KKLAFNPGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHGFHYII 120
QY 121 HELTOKTQDLKLSIGNTLFIIDQRLQPORKFLEDAKNFYSAETILTNFQNLMAQKQINDF 180

DB 121 HELTOKTQDLKLSIGNTLFIIDQRLQPORKFLEDAKNFYSAETILTNFQNLMAQKQINDF 180
QY 181 ISOCTHGKINNLINENIDPGTVMLANIYIFPRARWKHEFDPNVTKEEDFLEKNSSVKVP 240
DB 181 ISOCTHGKINNLINENIDPGTVMLANIYIFPRARWKHEFDPNVTKEEDFLEKNSSVKVP 240
QY 241 MFRSGIYQVGYDDKLSCTTILFIYQKNITAIPIIPDEGKLNLEKGLQVDFSRMKTLLS 300
DB 241 MFRSGIYQVGYDDKLSCTTILFIYQKNITAIPIIPDEGKLNLEKGLQVDFSRMKTLLS 300
QY 301 RRVVDVSVPLNHTGTFDCLKTSLYIGVSKIPIEBHGLTKIAPHRSIKVGEAVHAKELKM 360
DB 301 RRVVDVSVPLNHTGTFDCLKTSLYIGVSKIPIEBHGLTKIAPHRSIKVGEAVHAKELKM 360
QY 361 DERGTGAAGTGAGTLPMEETPLVVKIDKPYLLIYSBKIPSVLFLKIVNPICK 414
DB 361 DERGTGAAGTGAGTLPMEETPLVVKIDKPYLLIYSBKIPSVLFLKIVNPICK 414

RESULT 4

US-10-168-425-12
Sequence 12; Application US/10168425
Publication No. US20030124706A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: YANG, Junming
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BURBORD, Neil
APPLICANT: HU-YOUNG, Janice
APPLICANT: LU, Dying Aina M.
APPLICANT: REDDY, Roopa
APPLICANT: NGUYEN, Damien B.
APPLICANT: TANG, Y. Tom
APPLICANT: YAO, Monique G.
APPLICANT: LAU, Preeti
TITLE OF INVENTION: PROTEASES
FILE REFERENCE: PI-0003 PCT
CURRENT APPLICATION NUMBER: US/10/168,425
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/172,055; 60/177,334; 60/178,884; 60/179,903
PRIOR FILING DATE: 1999-12-23; 2000-01-21; 2000-01-28; 2000-02-02
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PERL Program
SEQ ID NO 12
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20030124706A1 7257324CD1
US-10-168-425-12

Query Match 100.0%; Score 414; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIPLAVILTVYKGLKPSFSPRNKALSEVQGMKORMAKELARQNDLGFKLL 60
DB 1 MNPTGLAIPLAVILTVYKGLKPSFSPRNKALSEVQGMKORMAKELARQNDLGFKLL 60
QY 61 KKLAFNPGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHGFHYII 120
DB 61 KKLAFNPGRNIFLSPISISTAFSMLCLGAQDSTLDEIKQGFNFRKMPKEDLHGFHYII 120
QY 121 HELTOKTQDLKLSIGNTLFIIDQRLQPORKFLEDAKNFYSAETILTNFQNLMAQKQINDF 180
DB 121 HELTOKTQDLKLSIGNTLFIIDQRLQPORKFLEDAKNFYSAETILTNFQNLMAQKQINDF 180
QY 181 ISOCTHGKINNLINENIDPGTVMLANIYIFPRARWKHEFDPNVTKEEDFLEKNSSVKVP 240
DB 181 ISOCTHGKINNLINENIDPGTVMLANIYIFPRARWKHEFDPNVTKEEDFLEKNSSVKVP 240

QY 241 MFRSGIYGVGDDKLSCTIIEIPYOKNITAFILPDEGKLKHLKGLQVDTFSRWKTLIS 300
|
|
|
Db 241 MFRSGIYGVGDDKLSCTIIEIPYOKNITAFILPDEGKLKHLKGLQVDTFSRWKTLIS 300
|
|
|
QY 301 RRVVDSVPRLLHMTGTFDLTKTSLYIGVSKIPEEHGDLTKIAPHRSLKVGSAVHKAELKM 360
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|
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Db 301 RRVVDSVPRLLHMTGTFDLTKTSLYIGVSKIPEEHGDLTKIAPHRSLKVGSAVHKAELKM 360
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QY 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLPLGKIIVNPIGK 414
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Db 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLPLGKIIVNPIGK 414
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RESULT 5

US-10-629-248-14
; Sequence 14, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tallon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/10/629,248
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/755,665
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-629-248-14

Query Match 100.0%; Score 414; DB 4; Length 414;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVALITVKGILKSPSPRNKALSEVQGMKQRMKAKEIARQNDLGFRL 60
|
|
|
Db 1 MNPTGLAIFLAVALITVKGILKSPSPRNKALSEVQGMKQRMKAKEIARQNDLGFRL 60
|
|
|
QY 61 KCLAFYVPGNIFLSPISISTAFSMLCLGAQDSTLDEIKGFNRKQPEKDLHGFHYII 120
|
|
|
Db 61 KCLAFYVPGNIFLSPISISTAFSMLCLGAQDSTLDEIKGFNRKQPEKDLHGFHYII 120
|
|
|
QY 121 HELTOKTQDLKLSIGNTLFIQRLQPORKFLDANKFYSAETIITNFQNLMAQKQINDF 180
|
|
|
Db 121 HELTOKTQDLKLSIGNTLFIQRLQPORKFLDANKFYSAETIITNFQNLMAQKQINDF 180
|
|
|
QY 121 HELTOKTQDLKLSIGNTLFIQRLQPORKFLDANKFYSAETIITNFQNLMAQKQINDF 180
|
|
|
Db 121 HELTOKTQDLKLSIGNTLFIQRLQPORKFLDANKFYSAETIITNFQNLMAQKQINDF 180
|
|
|
QY 181 ISOETHKINKNLINIDPGVLMLANIIFPRARKHEDPVTYBDFLEKNSVVKPM 240
|
|
|
Db 181 ISOETHKINKNLINIDPGVLMLANIIFPRARKHEDPVTYBDFLEKNSVVKPM 240
|
|
|
QY 241 MFRSGIYGVGDDKLSCTIIEIPYOKNITAFILPDEGKLKHLKGLQVDTFSRWKTLIS 300
|
|
|
Db 241 MFRSGIYGVGDDKLSCTIIEIPYOKNITAFILPDEGKLKHLKGLQVDTFSRWKTLIS 300
|
|
|
QY 301 RRVVDSVPRLLHMTGTFDLTKTSLYIGVSKIPEEHGDLTKIAPHRSLKVGSAVHKAELKM 360
|
|
|
Db 301 RRVVDSVPRLLHMTGTFDLTKTSLYIGVSKIPEEHGDLTKIAPHRSLKVGSAVHKAELKM 360
|
|
|
QY 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLPLGKIIVNPIGK 414
|
|
|
Db 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLPLGKIIVNPIGK 414
|
|
|

RESULT 6

US-10-629-248-55
; Sequence 55, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tallon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/10/629,248
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/755,665
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 55
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-629-248-55

Query Match 100.0%; Score 414; DB 4; Length 414;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVALITVKGILKSPSPRNKALSEVQGMKQRMKAKEIARQNDLGFRL 60
|
|
|
Db 1 MNPTGLAIFLAVALITVKGILKSPSPRNKALSEVQGMKQRMKAKEIARQNDLGFRL 60
|
|
|
QY 61 KCLAFYVPGNIFLSPISISTAFSMLCLGAQDSTLDEIKGFNRKQPEKDLHGFHYII 120
|
|
|
Db 61 KCLAFYVPGNIFLSPISISTAFSMLCLGAQDSTLDEIKGFNRKQPEKDLHGFHYII 120
|
|
|
QY 121 HELTOKTQDLKLSIGNTLFIQRLQPORKFLDANKFYSAETIITNFQNLMAQKQINDF 180
|
|
|
Db 121 HELTOKTQDLKLSIGNTLFIQRLQPORKFLDANKFYSAETIITNFQNLMAQKQINDF 180
|
|
|
QY 181 ISOETHKINKNLINIDPGVLMLANIIFPRARKHEDPVTYBDFLEKNSVVKPM 240
|
|
|
Db 181 ISOETHKINKNLINIDPGVLMLANIIFPRARKHEDPVTYBDFLEKNSVVKPM 240
|
|
|
QY 241 MFRSGIYGVGDDKLSCTIIEIPYOKNITAFILPDEGKLKHLKGLQVDTFSRWKTLIS 300
|
|
|
Db 241 MFRSGIYGVGDDKLSCTIIEIPYOKNITAFILPDEGKLKHLKGLQVDTFSRWKTLIS 300
|
|
|
QY 301 RRVVDSVPRLLHMTGTFDLTKTSLYIGVSKIPEEHGDLTKIAPHRSLKVGSAVHKAELKM 360
|
|
|
Db 301 RRVVDSVPRLLHMTGTFDLTKTSLYIGVSKIPEEHGDLTKIAPHRSLKVGSAVHKAELKM 360
|
|
|
QY 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLPLGKIIVNPIGK 414
|
|
|
Db 361 DERGTGAAGTGAOTLPMETPLVVKIDKPYLLIYSEKIPSVLPLGKIIVNPIGK 414
|
|
|

RESULT 7

US-10-629-248-56
; Sequence 56, Application US/10629248
; Publication No. US20040116671A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tallon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME

```

; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/10/629,248
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/755,665
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 56
; LENGTH: 414
; TYPE: PR
; ORGANISM: Homo sapiens
; US-10-629-248-56

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Query Match 100.0%; Score 414; DB 4; Length 414;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MNPFLGLAIFLAVLLTVKGLIKPSFSPRYKALSEVQWKORMAAKELARQNNDLGFKLL 60
DB 1 MNPFLGLAIFLAVLLTVKGLIKPSFSPRYKALSEVQWKORMAAKELARQNNDLGFKLL 60
QY 61 KKLAFNPGNITFLSPISITAFSMLCLGADSTLDEIKQGFNFRKMPKEDLHGGFYII 120
DB 61 KKLAFNPGNITFLSPISITAFSMLCLGADSTLDEIKQGFNFRKMPKEDLHGGFYII 120
QY 121 HELTQKTODLKLSIGNTLFIQRLQPKRFLBDANKFYSAEITLTFQNLMAQKQINDP 180
DB 121 HELTQKTODLKLSIGNTLFIQRLQPKRFLBDANKFYSAEITLTFQNLMAQKQINDP 180
QY 181 ISQKTHGKNNLIENIDPGTWMLLANYIFPRARKHGFDPNTKEDPFLKNSSVKVP 240
DB 181 ISQKTHGKNNLIENIDPGTWMLLANYIFPRARKHGFDPNTKEDPFLKNSSVKVP 240
QY 241 MFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLIS 300
DB 241 MFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLIS 300
QY 301 RRVVDVSVRLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSKVGSAVHKAELKM 360
DB 301 RRVVDVSVRLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSKVGSAVHKAELKM 360
QY 361 DERGTGAAGTGAQTLPMTETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPICK 414
DB 361 DERGTGAAGTGAQTLPMTETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPICK 414

```

RESULT 8

```

; Sequence 134, Application US/10012542
; Publication No. US20030044851A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532

```

```

; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PR
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino
; OTHER INFORMATION: acids
; US-10-012-542-134

```

Query Match 100.0%; Score 414; DB 4; Length 415;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MNPFLGLAIFLAVLLTVKGLIKPSFSPRYKALSEVQWKORMAAKELARQNNDLGFKLL 60
DB 1 MNPFLGLAIFLAVLLTVKGLIKPSFSPRYKALSEVQWKORMAAKELARQNNDLGFKLL 60
QY 61 KKLAFNPGNITFLSPISITAFSMLCLGADSTLDEIKQGFNFRKMPKEDLHGGFYII 120
DB 61 KKLAFNPGNITFLSPISITAFSMLCLGADSTLDEIKQGFNFRKMPKEDLHGGFYII 120
QY 121 HELTQKTODLKLSIGNTLFIQRLQPKRFLBDANKFYSAEITLTFQNLMAQKQINDP 180
DB 121 HELTQKTODLKLSIGNTLFIQRLQPKRFLBDANKFYSAEITLTFQNLMAQKQINDP 180
QY 181 ISQKTHGKNNLIENIDPGTWMLLANYIFPRARKHGFDPNTKEDPFLKNSSVKVP 240
DB 181 ISQKTHGKNNLIENIDPGTWMLLANYIFPRARKHGFDPNTKEDPFLKNSSVKVP 240
QY 241 MFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLIS 300
DB 241 MFRSGIYQGYDDKLSCTTLEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWKTLIS 300
QY 301 RRVVDVSVRLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSKVGSAVHKAELKM 360
DB 301 RRVVDVSVRLHMTGTFDLKKTLSYIGVSKIPEEHGDLTKIAPHRSKVGSAVHKAELKM 360
QY 361 DERGTGAAGTGAQTLPMTETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPICK 414
DB 361 DERGTGAAGTGAQTLPMTETPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPICK 414

```

RESULT 9

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; Sequence 134, Application US/10115123
; Publication No. US20030065151A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029G30AP1D2
; CURRENT APPLICATION NUMBER: US/10/115,123
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415

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;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (415)
;; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-115-123-134

Query Match 100.0%; Score 414; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVALITVYGLKLPSPSPRYKALSEVQGMKQMAKELARQMDLGFRL 60
DB 1 MNPTGLAIFLAVALITVYGLKLPSPSPRYKALSEVQGMKQMAKELARQMDLGFRL 60
QY 61 KCLAFYVPGNRIFLSPISISTAFSMLCLGADSTLDEIKQFNFRKPEKDLHGFIYI 120
DB 61 KCLAFYVPGNRIFLSPISISTAFSMLCLGADSTLDEIKQFNFRKPEKDLHGFIYI 120
QY 121 HELTQKODLKLSTIGNTLFDQRLQPKFLEDAKNFYSAETILTNPQNLMAQKQINDF 180
DB 121 HELTQKODLKLSTIGNTLFDQRLQPKFLEDAKNFYSAETILTNPQNLMAQKQINDF 180
QY 181 ISQTHGKINNLINIDPGTVMLLANYIFPRARKHEFDPNVTKBEDFLEKNSSVKVP 240
DB 181 ISQTHGKINNLINIDPGTVMLLANYIFPRARKHEFDPNVTKBEDFLEKNSSVKVP 240
QY 241 MFRSGIYQVGDYDQLSTIIEIPYQKNITAFILPDEGKLKHLKGLQVDFPSWKTLIS 300
DB 241 MFRSGIYQVGDYDQLSTIIEIPYQKNITAFILPDEGKLKHLKGLQVDFPSWKTLIS 300
QY 301 RRVVDVSPRLHMTGTDLKKTLSYIGVSKIPEHGLTITAPRSLKVGAAVKAELKM 360
DB 301 RRVVDVSPRLHMTGTDLKKTLSYIGVSKIPEHGLTITAPRSLKVGAAVKAELKM 360
QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGIIVNPIGK 414
DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGIIVNPIGK 414

RESULT 10
US-10-800-834-134
; Sequence 134, Application US/10800834
; Publication No. US20040146930A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1D3
; CURRENT APPLICATION NUMBER: US/10/800,834
; PRIOR FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: 10/115,123
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415

;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (415)
;; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-800-834-134

Query Match 100.0%; Score 414; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTGLAIFLAVALITVYGLKLPSPSPRYKALSEVQGMKQMAKELARQMDLGFRL 60
DB 1 MNPTGLAIFLAVALITVYGLKLPSPSPRYKALSEVQGMKQMAKELARQMDLGFRL 60
QY 61 KCLAFYVPGNRIFLSPISISTAFSMLCLGADSTLDEIKQFNFRKPEKDLHGFIYI 120
DB 61 KCLAFYVPGNRIFLSPISISTAFSMLCLGADSTLDEIKQFNFRKPEKDLHGFIYI 120
QY 121 HELTQKODLKLSTIGNTLFDQRLQPKFLEDAKNFYSAETILTNPQNLMAQKQINDF 180
DB 121 HELTQKODLKLSTIGNTLFDQRLQPKFLEDAKNFYSAETILTNPQNLMAQKQINDF 180
QY 181 ISQTHGKINNLINIDPGTVMLLANYIFPRARKHEFDPNVTKBEDFLEKNSSVKVP 240
DB 181 ISQTHGKINNLINIDPGTVMLLANYIFPRARKHEFDPNVTKBEDFLEKNSSVKVP 240
QY 241 MFRSGIYQVGDYDQLSTIIEIPYQKNITAFILPDEGKLKHLKGLQVDFPSWKTLIS 300
DB 241 MFRSGIYQVGDYDQLSTIIEIPYQKNITAFILPDEGKLKHLKGLQVDFPSWKTLIS 300
QY 301 RRVVDVSPRLHMTGTDLKKTLSYIGVSKIPEHGLTITAPRSLKVGAAVKAELKM 360
DB 301 RRVVDVSPRLHMTGTDLKKTLSYIGVSKIPEHGLTITAPRSLKVGAAVKAELKM 360
QY 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGIIVNPIGK 414
DB 361 DERGTGAAGTGAQTLPMETPLVVKIDKPYLLIYSEKIPSVLFLGIIVNPIGK 414

RESULT 11
US-09-755-665-57
; Sequence 57, Application US/09755665
; Patent No. US20020107186A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce B.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1) . (361)
; OTHER INFORMATION: Wherein Xaa is any amino acid as defined in the
; OTHER INFORMATION: specification
US-09-755-665-57

Query Match 74.9%; Score 310; DB 3; Length 361;
Best Local Similarity 100.0%; Pred. No. 4,2e-291;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 DLGFKLLKLLAFNPGNIFLSPISISTAFSMLCLGADSTLDEIRKGFNRKMPKEDLH 113
DB 1 DLGFKLLKLLAFNPGNIFLSPISISTAFSMLCLGADSTLDEIRKGFNRKMPKEDLH 60

QY 114 EGFHYIHELTKTODKLSIGNTLFDIDRLQPKRKELEDKXNFSATILLNFOULEMA 173
DB 61 EGFHYIHELTKTODKLSIGNTLFDIDRLQPKRKELEDKXNFSATILLNFOULEMA 120

QY 174 OKQINDFIQKTHGKINNLINENIDPGTVMLLANYIFPRARKHIEFDNNTKEEDFLEKN 233
DB 121 OKQINDFIQKTHGKINNLINENIDPGTVMLLANYIFPRARKHIEFDNNTKEEDFLEKN 180

QY 234 SSVKVPMMFRSGIYQGYDDKLSCTTLEIPYOKNITAIPIIPBEGKLEKGLQVDTFS 293
DB 181 SSVKVPMMFRSGIYQGYDDKLSCTTLEIPYOKNITAIPIIPBEGKLEKGLQVDTFS 240

QY 294 RMTLLSRVVDSVPRLHMTGTFDLKKTLSYIGVSKIFEBHGLTKIAPHRSKLVGEAV 353
DB 241 RMTLLSRVVDSVPRLHMTGTFDLKKTLSYIGVSKIFEBHGLTKIAPHRSKLVGEAV 300

QY 354 HKAEKXDER 363
DB 301 HKAEKXDER 310

RESULT 12

US-10-629-248-57
Sequence 57, Application US/10629248
Publication No. US2004011671A1
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhirdas K.
APPLICANT: Majumder, Kumud
APPLICANT: Tallon, Bruce E.
APPLICANT: Spaderma, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Macdougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/10/629,248
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/09/755,665
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
LENGTH: 361
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)..(361)
OTHER INFORMATION: wherein Xaa is any amino acid as defined in the
OTHER INFORMATION: specification
US-10-629-248-57

Query Match 74.9%; Score 310; DB 4; Length 361;
Best Local Similarity 100.0%; Pred. No. 4,2e-291;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 DLGFKLLKLLAFNPGNIFLSPISISTAFSMLCLGADSTLDEIRKGFNRKMPKEDLH 113
DB 1 DLGFKLLKLLAFNPGNIFLSPISISTAFSMLCLGADSTLDEIRKGFNRKMPKEDLH 60

QY 114 EGFHYIHELTKTODKLSIGNTLFDIDRLQPKRKELEDKXNFSATILLNFOULEMA 173
DB 61 EGFHYIHELTKTODKLSIGNTLFDIDRLQPKRKELEDKXNFSATILLNFOULEMA 120

QY 174 OKQINDFIQKTHGKINNLINENIDPGTVMLLANYIFPRARKHIEFDNNTKEEDFLEKN 233
DB 121 OKQINDFIQKTHGKINNLINENIDPGTVMLLANYIFPRARKHIEFDNNTKEEDFLEKN 180

DB 121 OKQINDFIQKTHGKINNLINENIDPGTVMLLANYIFPRARKHIEFDNNTKEEDFLEKN 180

QY 234 SSVKVPMMFRSGIYQGYDDKLSCTTLEIPYOKNITAIPIIPBEGKLEKGLQVDTFS 293
DB 181 SSVKVPMMFRSGIYQGYDDKLSCTTLEIPYOKNITAIPIIPBEGKLEKGLQVDTFS 240

QY 294 RMTLLSRVVDSVPRLHMTGTFDLKKTLSYIGVSKIFEBHGLTKIAPHRSKLVGEAV 353
DB 241 RMTLLSRVVDSVPRLHMTGTFDLKKTLSYIGVSKIFEBHGLTKIAPHRSKLVGEAV 300

QY 354 HKAEKXDER 363
DB 301 HKAEKXDER 310

RESULT 13

US-10-276-774-2202
Sequence 2202, Application US/10276774
Publication No. US20040053245A1
GENERAL INFORMATION:
APPLICANT: Hyabeg, Inc.
APPLICANT: Tang, Y. Tom et al
TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-030
CURRENT APPLICATION NUMBER: US/10/276,774
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 2700
SOFTWARE: Custom
SEQ ID NO 2202
LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens
US-10-276-774-2202

Query Match 43.7%; Score 181; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 3,8e-166;
Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NMPTGLAIFLAVLLTVKGLKPSFSPNNYKALSEVQKQMAAKELARQNDLGFKLL 60
DB 18 NMPTGLAIFLAVLLTVKGLKPSFSPNNYKALSEVQKQMAAKELARQNDLGFKLL 77

QY 61 KCLAFNPGNIFLSPISISTAFSMLCLGADSTLDEIRKGFNRKMPKEDLHEGFHYII 120
DB 78 KCLAFNPGNIFLSPISISTAFSMLCLGADSTLDEIRKGFNRKMPKEDLHEGFHYII 137

QY 121 HELTKTODKLSIGNTLFDIDRLQPKRKELEDKXNFSATILLNFOULEMAOKQINDF 180
DB 138 HELTKTODKLSIGNTLFDIDRLQPKRKELEDKXNFSATILLNFOULEMAOKQINDF 197

QY 181 I 181
DB 198 I 198

RESULT 14

US-09-864-761-48438
Sequence 48438, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmics-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23

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; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 48438
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL132708.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: SWISSPROT HIT: P50447, EVALU8 8.00e-28
; OTHER INFORMATION: EST_HUMAN HIT: AV649144.1, EVALU8 3.00e-27
; US-09-864-761-48438

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Query Match          31.2%; Score 129; DB 3; Length 140;
Best Local Similarity 100.0%; Pred. No. 3e-116;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      83  FSWLCLGADSTLDEIKOGFNFRKMPKDIHSGFYIHELTKOTDCLKISGNTLFTDQ 142
DB      1  FSWLCLGADSTLDEIKOGFNFRKMPKDIHSGFYIHELTKOTDCLKISGNTLFTDQ 60

QY      143 RLOPORRPLEDANFYSAETILTNPONTLEMAKOKINDPISQKTHGKINNIENIDPQTM 202
DB      61  RLOPORRPLEDANFYSAETILTNPONTLEMAKOKINDPISQKTHGKINNIENIDPQTM 120

QY      203 LLANYIFPR 211
DB      121 LLANYIFPR 129

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Search completed: March 31, 2006, 10:13:53
 Job time : 121.26 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 31, 2006, 10:10:05 ; Search time 16.8875 Seconds
(without alignments)
746.288 Million cell updates/sec

Title: US-10-664-356-1562

Perfect score: 414

Sequence: 1 MNPTLGIATFLAVLLTVKGL.....YSEKIPSVLFLGKIVNPIGK 414

Scoring matrix: BLO62

Gapop 60.0 , Gapext 60.0

Searched: 180808 seqs, 30441898 residues

Word size: 35

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database :

- Published Applications_A New:
- 1: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 2: /SIDS5/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 3: /SIDS5/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 4: /SIDS5/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 5: /SIDS5/ptodata/2/pubpaa/US05_NEW_PUB.pep.*
 - 6: /SIDS5/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 7: /SIDS5/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 8: /SIDS5/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description

No matches found

Search completed: March 31, 2006, 10:14:30
Job time : 16.8875 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 31, 2006, 09:54:55 ; Search time 210.927 Seconds
(without alignments)
822.818 Million cell updates/sec

Title: US-10-664-356-1562_COPY_20_414
Perfect score: 395
Sequence: 1 LTKPSFSPRYKALSEVQGW.....YSEKIPSVLFGKIVNPIGK 395

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size: 15

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database :

- 1: A_Geneseq_21:*
- 2: geneseqp1980s:*
- 3: geneseqp1990s:*
- 4: geneseqp2000s:*
- 5: geneseqp2001s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	395	100.0	414	AAU05754	AAU05754 Human NOV
2	395	100.0	414	AAE04885	AAE04885 Human pro
3	395	100.0	414	ADA57300	ADA57300 Human sec
4	395	100.0	414	ADA41179	ADA41179 Human sec
5	395	100.0	414	ADN05952	ADN05952 Antipsoi
6	395	100.0	415	AAV86217	AAV86217 Human sec
7	395	100.0	415	ABO53360	ABO53360 Novel hum
8	334	84.6	414	AAU05759	AAU05759 Human pro
9	310	78.5	358	AAU05759	AAU05759 Human NOV
10	170	43.0	431	ABBI1832	ABBI1832 Human sec
11	170	43.0	431	AAW79882	AAW79882 Human pro
12	129	32.7	140	AAW70426	AAW70426 Human bon

ALIGNMENTS

RESULT 1

AAU05754 standard; protein; 414 AA.

AAU05754;

24-OCT-2001 (first entry)

XX	Human NOV polypeptide.
DE	
XX	Human; NOV7; AL132990 B; fertility disorder; spermatogenesis; cardiac;
XX	cytostatic; immunomodulatory; antiproliferative; antidiabetic;
KW	cell proliferation; cancer; diabetic retinopathy; angiogenic disorder;
KW	pulmonary disorder; haematopoietic disorder; immunological disorder;
KW	inflammatory disorder; tumour related disorders; emphysema; cirrhosis;
KW	wound healing; gene therapy.
XX	
OS	Homo sapiens.
XX	
XX	MO200149729-A2.
XX	
XX	12-JUL-2001.
XX	
XX	05-JAN-2001; 2001WO-US000299.
XX	
XX	06-JAN-2000; 2000US-0174724P.
XX	11-JAN-2000; 2000US-0175434P.
XX	11-JAN-2000; 2000US-0175488P.
XX	12-JAN-2000; 2000US-0175696P.
XX	12-JAN-2000; 2000US-0175743P.
XX	13-JAN-2000; 2000US-0175819P.
XX	07-AUG-2000; 2000US-0223524P.
XX	04-JAN-2001; 2001US-0075565S.
XX	
XX	(CURA-) CURAGEN CORP.
XX	
XX	Prayaga SK, Majumder K, Tallon BE, Spaderna SK, Spytek KA;
XX	MacDougall J;
XX	
XX	WPI, 2001-418356/44.
XX	N-PSDB; AAS10874.
XX	
XX	Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful
XX	for treating a syndrome associated with a NOVX-associated disorder, e.g.
XX	cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or
XX	pulmonary disorder.
XX	
XX	Claim 1; Page 32; 14pp; English.
XX	
XX	The invention relates to nucleic acids encoding NOVX (X being an integer
XX	from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
XX	useful in diagnosing, treating or manufacturing a medicament for a
XX	disease or disorder associated with NOVX e.g. cell proliferation (cancer
XX	and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
XX	disorders (e.g. of spermatogenesis), haematopoietic, immunological,
XX	inflammatory and tumour related disorders, emphysema, cirrhosis, wound
XX	healing. NOVX nucleic acids are also useful in gene therapy. They are
XX	also used for screening for a modulator of activity or of latency or
XX	predisposition to a NOVX-associated disorder. They are also useful for
XX	determining the presence of or predisposition to a NOVX-associated
XX	disorder. The present sequence represents NOV7 (AL132990 B), which has
XX	sequence homology to an unidentified human secreted protein (HMHGUS54)
XX	and to alpha anti-trypsin
XX	
XX	Sequence 414 AA:
XX	
XX	Query Match 100.0%; Score 395; DB 4; Length 414;
XX	Best Local Similarity 100.0%; Pred. No. 0;
XX	Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	
XX	1 LTKPSFSPRYKALSEVQGWKQMAKELARQNDLGFKLKKLAAPNPGNIFLSPISI 60
XX	20 LTKPSFSPRYKALSEVQGWKQMAKELARQNDLGFKLKKLAAPNPGNIFLSPISI 79
XX	
XX	61 STAFSMLCIGAQNSTIDEIKQGNFRKMPKDLHSGFHTIHLTKOTDLSIGNTLF 120
XX	80 STAFSMLCIGAQNSTIDEIKQGNFRKMPKDLHSGFHTIHLTKOTDLSIGNTLF 139
XX	
XX	121 IDQRLQRFLEDAKQFSAETITLTFQNLMAQKQINDFISQKHGKINLNINIDPG 180


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Db      140 IDQRLQPRKFLBDANKFSAETILTNPQNLMAQKQINDFISQKTHGKINNLINENIDPG 199
Qy      181 TWMLANTYFFRARMKHEFDPPNTKEDPFLKNSSVKVPMMFRSGIYQVYDDKLSCTI 240
Db      200 TWMLANTYFFRARMKHEFDPPNTKEDPFLKNSSVKVPMMFRSGIYQVYDDKLSCTI 259
Qy      241 LEIPYOKNTTAIFILPDEGKLKLEKGLQVDTFSRWKTLISRVDVSVPRLMHTGTFDL 300
Db      260 LEIPYOKNTTAIFILPDEGKLKLEKGLQVDTFSRWKTLISRVDVSVPRLMHTGTFDL 319
Qy      301 KKTLSYIGVSKIFEEHGDITKIAPHRSILKVGSAVHKAELKMDERGTGGAAGTGLPME 360
Db      320 KKTLSYIGVSKIFEEHGDITKIAPHRSILKVGSAVHKAELKMDERGTGGAAGTGLPME 379
Qy      361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
Db      380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414

RESULT 2
AAE04885
ID      AAE04885 standard; protein; 414 AA.
XX
AC      AAE04885;
XX
DT      10-SEP-2001 (first entry)
XX
DE      Human protease protein-12 (PRTS-12).
XX
KW      Human; protease protein-12; PRTS-12; cytostatic; hypotensive; antiviral;
KW      gastrointestinal disorder; anorexia; dysphagia; cardiovascular disorder;
KW      atherosclerosis; vasculitis; autoimmune disorder; inflammatory disorder;
KW      Alzheimer's disease; cell proliferative disorder; dermatitis; cirrhosis;
KW      acquired immune deficiency syndrome; AIDS; neurological disorder; asthma;
KW      developmental disorder; epithelial disorder; eczema; dementia; noctropic;
KW      neurological disorder; reproductive disorder; infertility; teratogenesis;
KW      immunosuppressive; drug screening; actinic keratosis; cardiac; epilepsy;
KW      anaemia; antitumour; gene therapy; antibacterial.
XX
OS      Homo sapiens.
XX
FH      Key Location/Qualifiers
FT      Peptide 1..19
FT      Protein /label= Signal_peptide 20..414
FT      Protein /note= "Mature human PRTS-12"
XX
PN      WO200146443-A2.
XX
PD      28-JUN-2001.
XX
PF      19-DEC-2000; 2000MO-US034811.
XX
PR      23-DEC-1999; 99US-0172055P.
PR      21-JAN-2000; 2000US-0177334P.
PR      28-JAN-2000; 2000US-0178884P.
PR      02-FEB-2000; 2000US-0179903P.
XX
PA      (INCY-) INCYTE GENOMICS INC.
XX
PI      Yang J, Baughn MR, Burford N, Au-Young J, Lu DM, Reddy R;
PI      Yue H, Nguyen DB, Tang YT, Yao MG, Lal P;
XX
DR      WPI: 2001-418080/44.
DR      N-PSDB; AAD09549.
XX
PT      Novel human protease proteins (PRTS) useful for diagnosing, treating,
PT      preventing gastrointestinal, cardiovascular, autoimmune/inflammatory,
PT      cell proliferative disorders associated with abnormal expression of PRTS.
XX
PS      Claim 1, Page 118, 129pp; English.
XX
CC      The present sequence is human protease protein (PRTS-12). Human PRTS and

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CC      its nucleic acid molecule are useful for the diagnosis, treatment and
CC      prevention of disorders associated with increased or decreased expression
CC      of PRTS. Examples of such disorders include, gastrointestinal disorder
CC      such as anorexia, dysphagia; cardiovascular disorder such as
CC      atherosclerosis, vasculitis; autoimmune/inflammatory disorder such as
CC      acquired immune deficiency syndrome (AIDS), asthma; cell proliferative
CC      disorder such as actinic keratosis, cirrhosis; developmental disorder
CC      such as epilepsy, anaemia; epithelial disorder such as allergic contact
CC      dermatitis, eczema; neurological disorder such as Alzheimer's disease,
CC      dementia and reproductive disorder such as infertility and teratogenesis.
CC      PRTS DNA is useful for creating 'knockin' humanised animals (pigs) or
CC      transgenic animals (mice or rats) to model human disease. PRTS DNA is
CC      also in useful in gene therapy. PRTS and its immunogenic fragments are
CC      useful for screening libraries of compounds in several drug screening
CC      assays. PRTS is useful for analysing the proteome of a tissue or cell
CC      type
XX
SQ      Sequence 414 AA;
XX
Query Match      100.0%; Score 395; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LKPSFSPNNYKQLSEVQGWKQPMKAEIARQNDLGFLLKLAFFNPGNIPLSLI 60
Db      20 LKPSFSPNNYKQLSEVQGWKQPMKAEIARQNDLGFLLKLAFFNPGNIPLSLI 79
Qy      61 STAFSMLCLGAQDSTLDEIKQGFNFRKMPKOLHGFHYIHELQKQODLKLSGNTLF 120
Db      80 STAFSMLCLGAQDSTLDEIKQGFNFRKMPKOLHGFHYIHELQKQODLKLSGNTLF 139
Qy      121 IDQRLQPRKFLBDANKFSAETILTNPQNLMAQKQINDFISQKTHGKINNLINENIDPG 180
Db      140 IDQRLQPRKFLBDANKFSAETILTNPQNLMAQKQINDFISQKTHGKINNLINENIDPG 199
Qy      181 TWMLANTYFFRARMKHEFDPPNTKEDPFLKNSSVKVPMMFRSGIYQVYDDKLSCTI 240
Db      200 TWMLANTYFFRARMKHEFDPPNTKEDPFLKNSSVKVPMMFRSGIYQVYDDKLSCTI 259
Qy      241 LEIPYOKNTTAIFILPDEGKLKLEKGLQVDTFSRWKTLISRVDVSVPRLMHTGTFDL 300
Db      260 LEIPYOKNTTAIFILPDEGKLKLEKGLQVDTFSRWKTLISRVDVSVPRLMHTGTFDL 319
Qy      301 KKTLSYIGVSKIFEEHGDITKIAPHRSILKVGSAVHKAELKMDERGTGGAAGTGLPME 360
Db      320 KKTLSYIGVSKIFEEHGDITKIAPHRSILKVGSAVHKAELKMDERGTGGAAGTGLPME 379
Qy      361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
Db      380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414

RESULT 3
ADA57300
ID      ADA57300 standard; protein; 414 AA.
XX
AC      ADA57300;
XX
DT      20-NOV-2003 (first entry)
XX
DE      Human secreted protein #583.
XX
KW      immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW      cytostatic; cerebroprotective; neuroprotective; noctropic;
KW      cardiovascular; antiarteriosclerotic; gene therapy;
KW      human secreted protein; immune disorder; inflammation;
KW      respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW      inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW      multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW      Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW      triple helix formation; antisense gene therapy; forensic biology.
XX
OS      Homo sapiens.

```

XX MO2002102994-A2.
 XX 27-DEC-2002.
 XX 19-MAR-2002; 2002MO-US008278.
 XX 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM;
 XX WPI; 2003-167512/16.
 DR N-PSDB; ADA56404.
 XX
 PT New human secreted polypeptides and polynucleotides, useful for
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
 PT conditions, respiratory disorders, cancers, CNS disorders, or
 PT neurodegenerative disorders.
 PS
 PS Claim 13; SEQ ID NO 1490; 1754pp; English.
 XX
 CC The invention relates to 592 new human secreted polypeptides useful for
 CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
 CC conditions, respiratory disorders, cancers, CNS disorders, or
 CC neurodegenerative disorders, or polypeptides comprising an amino acid
 CC sequence at least 95% identical to the new sequences. The polypeptides,
 CC antibodies or antibody fragments that bind to the polypeptides, nucleic
 CC acids encoding the polypeptides, agonists or antagonists that binds to
 CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
 CC compositions for diagnosing, treating or preventing an e.g. immune
 CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
 CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
 CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
 CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
 CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
 CC polynucleotides are useful for chromosome identification, chromosome
 CC mapping, for controlling gene expression through triple helix formation
 CC or antisense DNA or RNA, in gene therapy, for identifying individuals
 CC from minute biological samples, in forensic biology, and as hybridization
 CC probes. The polypeptides are useful for as molecular weight markers on
 CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
 CC gels, to raise antibodies, for testing biological activities, and for
 CC treating or preventing neural disorders, immune system disorders,
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal, proliferative and/or cancerous diseases. This sequence corresponds
 CC to one of the polypeptide of the invention. Note: This sequence corresponds
 CC to this patent did form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 414 AA:
 SQ
 Query Match 100.0%; Score 395; DB 6; Length 414;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 181 TWLNLANYIFRRARMKHEPDPNTYKEDPFLERKNSVYKVMRMSGIYQVGDYDKLSCTI 240
 DB 200 TWLNLANYIFRRARMKHEPDPNTYKEDPFLERKNSVYKVMRMSGIYQVGDYDKLSCTI 259
 QY 241 LEIPYQKNITATITLPDEGLKLEKGLQYDTSRKTTLSRRVDSVRLMHTGTFDL 300
 DB 260 LEIPYQKNITATITLPDEGLKLEKGLQYDTSRKTTLSRRVDSVRLMHTGTFDL 319
 QY 301 KKTLSYGVSKIFEEHGDLTAKIAPHRSILKYGAVHKAELKMDRSGTEGAAGTGAQTLPM 360
 DB 320 KKTLSYGVSKIFEEHGDLTAKIAPHRSILKYGAVHKAELKMDRSGTEGAAGTGAQTLPM 379
 QY 361 TPLVVKIDKPEYLLIYSEKIPSVLFLGKIYVPIGK 395
 DB 380 TPLVVKIDKPEYLLIYSEKIPSVLFLGKIYVPIGK 414
 RESULT 4
 ADA41179
 ID ADA41179 standard; protein; 414 AA.
 XX
 AC ADA41179;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human secreted protein.
 XX
 KW Human; secreted protein; cancer; hyperproliferative disorder;
 KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
 KW anaemia; allergic reaction; asthma; cardiovascular disorder;
 KW wound healing; cystostatic; immunosuppressive; nocotropic; neuroprotective;
 KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
 KW vulnereary; cardiac; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN MO2002102993-A2.
 XX
 PD 27-DEC-2002.
 XX
 PF 19-MAR-2002; 2002MO-US008123.
 XX
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM;
 XX WPI; 2003-175238/17.
 DR
 XX
 PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing,
 PT preventing or treating cancer or other hyperproliferative disorder,
 PT asthma, allergies or AIDS.
 XX
 XX Claim 1; SEQ ID NO 1561; 3205pp; English.
 PS
 PS The invention relates to novel genes ADA39629-ADA40565 and proteins
 CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
 CC treating or ameliorating medical conditions e.g. by protein or gene
 CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
 CC fragments, and agonists or antagonists that bind to the polypeptide are
 CC useful for preparing a diagnostic or pharmaceutical composition for
 CC diagnosing or treating cancer or other hyperproliferative disorder. The
 CC polypeptides and nucleic acid molecules are also useful for detecting,
 CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
 CC or other hyperproliferative disorders including neoplasms, autoimmune
 CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
 CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
 CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
 CC thrombocytopenia), allergic reactions including asthma or eczema,

CC Inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 414 AA;

Query Match 100.0%; Score 395; DB 6; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPSFSPRYKALSEVQGMKQMAKELARQNMDFGLKKLAFYNGRNIPLSPLSI 60
DB LKPSFSPRYKALSEVQGMKQMAKELARQNMDFGLKKLAFYNGRNIPLSPLSI 79
QY 61 STAFSMLCIGAODSTLDEIKQGFNFRKMPKEDLHEGFHYIHELTKQTDKLKISGNTLF 120
DB STAFSMLCIGAODSTLDEIKQGFNFRKMPKEDLHEGFHYIHELTKQTDKLKISGNTLF 139
QY 121 IDORLOPQKRFEDAKNFSAETITLNFQNLMAQKQINDFISQTHGKINNLINENIDPG 180
DB IDORLOPQKRFEDAKNFSAETITLNFQNLMAQKQINDFISQTHGKINNLINENIDPG 199
QY 181 TWMLANTYFFPRARMKHEPDNVTKEEDFLEKNSSVKVPMMFRSGIYOVGYDDKLSCTI 240
DB TWMLANTYFFPRARMKHEPDNVTKEEDFLEKNSSVKVPMMFRSGIYOVGYDDKLSCTI 259
QY 241 LEIPYQKNITAFILPDEGKLKHEKGLQVDTFSRWKTLISRNVDSVPRLLMTGTFDL 300
DB LEIPYQKNITAFILPDEGKLKHEKGLQVDTFSRWKTLISRNVDSVPRLLMTGTFDL 319
QY 301 KKTLSYIGVSKIFEEHGDLTAKIAPHRSLSKVGEAVHKAELKMDERGTEGAAGTGLPME 360
DB KKTLSYIGVSKIFEEHGDLTAKIAPHRSLSKVGEAVHKAELKMDERGTEGAAGTGLPME 379
QY 361 TPLVVKIDKPYLLIYSEKIPSVLFLGKIIVPIGK 395
DB TPLVVKIDKPYLLIYSEKIPSVLFLGKIIVPIGK 414

RESULT 5
ADN05952
ID ADN05952 standard; protein; 414 AA.

AC ADN05952;
DT 01-JUL-2004 (first entry)

DE Antipsoriatic protein sequence #1136.

KW antipsoriatic; gene therapy; psoriasis; diagnosis.

XX Homo sapiens.

XX WO2004028479-A2.

XX 08-APR-2004.

XX 25-SEP-2003; 2003WO-US030907.

XX 25-SEP-2002; 2002US-0414006P.

XX (GENTH) GENENTECH INC.

XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
PI Wu TD;
XX
XX WPI; 2004-305105/28.
DR N-PSDB; ADN05951.

PT New PRO nucleic acid or polypeptide, useful for preparing a
PT pharmaceutical composition for diagnosing or treating psoriasis in a
PT mammal.

PS Claim 9; SEQ ID NO 2347; 3069pp; English.

CC The invention relates to novel polynucleotide and polypeptides for
CC treating psoriasis or a sequence having at least 80% identity to the
CC above sequences. The nucleic acid is useful for preparing a composition
CC for diagnosing or treating psoriasis in a mammal. This sequence
CC corresponds to one of the polypeptides of the invention.

SQ Sequence 414 AA;

Query Match 100.0%; Score 395; DB 8; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPSFSPRYKALSEVQGMKQMAKELARQNMDFGLKKLAFYNGRNIPLSPLSI 60
DB LKPSFSPRYKALSEVQGMKQMAKELARQNMDFGLKKLAFYNGRNIPLSPLSI 79
QY 61 STAFSMLCIGAODSTLDEIKQGFNFRKMPKEDLHEGFHYIHELTKQTDKLKISGNTLF 120
DB STAFSMLCIGAODSTLDEIKQGFNFRKMPKEDLHEGFHYIHELTKQTDKLKISGNTLF 139
QY 121 IDORLOPQKRFEDAKNFSAETITLNFQNLMAQKQINDFISQTHGKINNLINENIDPG 180
DB IDORLOPQKRFEDAKNFSAETITLNFQNLMAQKQINDFISQTHGKINNLINENIDPG 199
QY 181 TWMLANTYFFPRARMKHEPDNVTKEEDFLEKNSSVKVPMMFRSGIYOVGYDDKLSCTI 240
DB TWMLANTYFFPRARMKHEPDNVTKEEDFLEKNSSVKVPMMFRSGIYOVGYDDKLSCTI 259
QY 241 LEIPYQKNITAFILPDEGKLKHEKGLQVDTFSRWKTLISRNVDSVPRLLMTGTFDL 300
DB LEIPYQKNITAFILPDEGKLKHEKGLQVDTFSRWKTLISRNVDSVPRLLMTGTFDL 319
QY 301 KKTLSYIGVSKIFEEHGDLTAKIAPHRSLSKVGEAVHKAELKMDERGTEGAAGTGLPME 360
DB KKTLSYIGVSKIFEEHGDLTAKIAPHRSLSKVGEAVHKAELKMDERGTEGAAGTGLPME 379
QY 361 TPLVVKIDKPYLLIYSEKIPSVLFLGKIIVPIGK 395
DB TPLVVKIDKPYLLIYSEKIPSVLFLGKIIVPIGK 414

RESULT 6
AAH6217
ID AAH6217 standard; protein; 415 AA.

AC AAH6217;

DT 19-APR-2000 (first entry)

DE Human secreted protein HMHG54, SEQ ID NO:132.

KW Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW therapy.

XX Homo sapiens.

XX PN KO9966041-A1.
 XX 23-DEC-1999.
 XX
 XX PF 15-JUN-1999; 99MO-US013418.
 XX 16-JUN-1998; 98US-0089507P.
 XX 16-JUN-1998; 98US-0089508P.
 XX 16-JUN-1998; 98US-0089509P.
 XX 16-JUN-1998; 98US-0089510P.
 XX 22-JUN-1998; 98US-0090112P.
 XX 22-JUN-1998; 98US-0090113P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Ni J, Rosen CA, Wei Y, Young PE, Florence KA,
 PI Soppet DR, Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R,
 PI Lafleur DW, Olsen HS, Shi Y, Moore PA, Komatsoulis G;
 XX
 XX MPI; 2000-106100/09.
 DR N-PSDB; AA297021.
 XX
 PT New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders.
 XX
 XX Claim 1; Page 389-390; 586pp; English.
 PS
 XX AA297019 to AA297137 represent 94 isolated human secreted protein genes.
 CC AA297019 to AA297137 are the secreted proteins encoded by the 94 human
 CC genes. This sequence represents a fragment of one of the human secreted
 CC proteins. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions, e.g.,
 CC by protein or gene therapy. Also pathological conditions can be diagnosed
 CC by determining the amount of the new polypeptides in a sample or by
 CC determining the presence of mutations in the new genes. Specific uses are
 CC described for each of the 94 genes, based on which tissues they are most
 CC highly expressed in, and include developing products for the diagnosis or
 CC treatment of cancer, tumours, developmental abnormalities and foetal
 CC deficiencies, blood disorders, diseases of the immune system, autoimmune
 CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
 CC schistosomiasis, arthritis, asthma, peoriasis, sepsis, skin disorders,
 CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
 CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
 CC also useful for identifying their binding partners. The sequences shown
 CC in AA297019 to AA297137 represent fragments of the secreted proteins
 CC
 XX
 SQ Sequence 415 AA;

QY 301 KKTLSYIGVSKIPFEHDLTKIAPHRSKXGVAHVKAELKMDERGTGAAGTQTPME 360
 |||||
 Db 320 KKTLSYIGVSKIPFEHDLTKIAPHRSKXGVAHVKAELKMDERGTGAAGTQTPME 379
 |||||
 QY 361 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYNPICK 395
 |||||
 Db 380 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYNPICK 414
 |||||
 RESULT 7
 ID ABO53360 standard; protein; 415 AA.
 XX
 AC ABO53360;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Novel human secreted protein #3.
 XX
 KW Human; vaccine; immune system disorder; haematopoietic cell disorder;
 KW cancer; autoimmune disorder; rheumatoid arthritis; glomerulonephritis;
 KW HIV infection; anaemia; thrombocytopenia blood coagulation disorder;
 KW blood platelet disorder; wound; heart attack; myocardial infarction;
 KW stroke; scarring; asthma; graft-versus host rejection; inflammation;
 KW hyperproliferative disorder; lymphoproliferative disorder; arrhythmia;
 KW aberrant cellular division; cell proliferative disorder; angiogenesis;
 KW cardiovascular disorder; pulmonary heart disease; neovascularisation;
 KW hypertrophic scar; keloid; ocular disorder; diabetic retinopathy;
 KW uveitis; epithelial cell proliferation; neurological disease; apoptosis;
 KW Parkinson's disease; Alzheimer's disease; Huntington's chorea; AIDS; AIDS;
 KW anorectic lateral sclerosis; toxin induced liver disease; septic shock;
 KW cachexia; anorexia; lung damage; infection.
 XX
 OS Homo sapiens.
 XX
 XX US2003065151-A1.
 PN
 XX 03-APR-2003.
 PD
 XX
 XX 04-APR-2002; 2002US-00115123.
 PF
 XX 16-JUN-1998; 98US-0089507P.
 XX 16-JUN-1998; 98US-0089508P.
 XX 16-JUN-1998; 98US-0089509P.
 XX 16-JUN-1998; 98US-0089510P.
 XX 22-JUN-1998; 98US-0090112P.
 XX 22-JUN-1998; 98US-0090113P.
 XX 15-JUN-1999; 99MO-US013418.
 XX 14-DEC-1999; 99US-00461325.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Ni J, Rosen CA, Wei Y, Young P, Florence K, Soppet DR,
 PI Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R, Lafleur DW,
 PI Olsen H, Shi Y, Moore PA, Komatsoulis G;
 XX
 XX MPI; 2003-531736/50.
 DR N-PSDB; ACH66650.
 XX
 PT Novel antibody that binds specifically to a HCE3069 protein, useful for
 PT detecting the presence of a protein in a biological sample, and for
 PT treating cancers, autoimmune disorders and HIV infection.
 XX
 XX Disclosure; SEQ ID NO 134; 176pp; English.
 XX
 XX The invention relates to an isolated antibody or its fragment that
 XX specifically binds to a protein. The antibody is useful for detecting a
 XX protein in a biological sample, by contacting the biological sample with
 XX the antibody or its fragment and detecting the protein in the biological
 XX sample. The antibody is useful for purifying, detecting and targeting the
 XX human secreted proteins, including both in vitro and in vivo diagnostic
 XX and therapeutic methods. The antibody is useful for immunophenotyping of

cell lines in biological samples and in antibody-based therapies for treating, inhibiting and preventing diseases, disorders or conditions associated with aberrant expression and/or activity of the above proteins. The antibody is useful for treating deficiencies or disorders of immune system and haematopoietic cells, for increasing differentiation and proliferation of haematopoietic cells, for treating immune deficiencies or disorders e.g. cancers, autoimmune disorders (such as rheumatoid arthritis and glomerulonephritis), HIV infection, anaemia and thrombocytopenia and as a marker for a particular immune system disease or disorder. The antibody is also useful for treating blood coagulation disorders, blood platelet disorders, wounds, heart attacks (infarction), strokes, bearing and asthma. The antibody is also useful for treating or preventing graft-versus host rejection, for modulating inflammation, for treating hyperproliferative disorders e.g. lymphoproliferative disorders and cancers, for inhibiting aberrant cellular division and for treating cell proliferative disorders. The antibody is also useful for treating cardiovascular disorders e.g. pulmonary heart disease and arrhythmia, disorders associated with neovascularisation and angiogenesis, for treating hypertrophic scars and keloids, ocular disorders e.g. diabetic retinopathy and uveitis, for wound healing and disorders of epithelial cell proliferation. The antibody is also useful for treating neurological diseases e.g. Parkinson's disease, Alzheimer's disease, Huntington's chorea and amyotrophic lateral sclerosis (ALS), diseases associated with increased apoptosis e.g. AIDS, toxin induced liver disease, septic shock, cachexia and anorexia, for preventing and healing damage to lungs and for treating infectious diseases. The present sequence represents the amino acid sequence of a novel human secreted protein. Note: the sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?docId=20030065151

Sequence 415 AA;

Query Match 100.0%; Score 395; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 LKPSFSPNNYKALSEVOGKQMAKELARQNDLGFLLKCLAFYVNGRNIFLSPLSI 60
DB 20 LKPSFSPNNYKALSEVOGKQMAKELARQNDLGFLLKCLAFYVNGRNIFLSPLSI 79
QY 61 STAFSMLCIGADSTLDEIKQGFNRKMPKOLHGFHYIHELTKQODKLSTGNTLF 120
DB 80 STAFSMLCIGADSTLDEIKQGFNRKMPKOLHGFHYIHELTKQODKLSTGNTLF 139
QY 121 IDORLOPQRKFLBDANKFYSAETILTNFQNLMAQKQINDFISQKTHKINNLINIDPG 180
DB 140 IDORLOPQRKFLBDANKFYSAETILTNFQNLMAQKQINDFISQKTHKINNLINIDPG 199
QY 181 TWMLANTYIFFRARWKEHEDPNTVTEDEPFLEKNSSVKYPMMFRSGIYQGYDDKLSCTI 240
DB 200 TWMLANTYIFFRARWKEHEDPNTVTEDEPFLEKNSSVKYPMMFRSGIYQGYDDKLSCTI 259
QY 241 LEIPYOKNTTAIFILPDEGKLKLEKGLQVDTFSRKTTLSRRVVDVSPRLHMTCTFPL 300
DB 260 LEIPYOKNTTAIFILPDEGKLKLEKGLQVDTFSRKTTLSRRVVDVSPRLHMTCTFPL 319
QY 301 KKTLSYIGVSKTPEEHGDLTKIAPHRSLSYGEAVHAEIKMDRGEGAGAGTLPME 360
DB 320 KKTLSYIGVSKTPEEHGDLTKIAPHRSLSYGEAVHAEIKMDRGEGAGAGTLPME 379
QY 361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 395
DB 380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIVNPIGK 414

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RESULT 8
AAM78898
ID AAM78898 standard; protein; 414 AA.
AC AAM78898;
XX
DT 06-NOV-2001 (first entry)

Human protein SEQ ID NO 1560.
Human; cytokine; cell proliferation; cell differentiation; gene therapy;
vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation.
Homo sapiens.
MO200157190-A2.
09-AUG-2001.
05-FEB-2001; 2001WO-US004098.
03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
19-JUL-2000; 2000US-00620325.
01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-00663561.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
(HYSB-) HYSBQ INC.
Tang YF, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Xue AJ, Yang Y, Wejhrman T, Goodrich R;
WPI; 2001-476283/51.
N-PSDB; AAK52031.
Nucleic acids encoding polypeptides with cytokine-like activities, useful
in diagnosis and gene therapy.
Claim 20; Page 3878-3879; 6221pp; English.
The invention relates to polynucleotides (AAK51456-AAK53435) and the
encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
cytokine, cell proliferation or cell differentiation or which may induce
production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication

Sequence 414 AA;

Query Match 84.6%; Score 334; DB 4; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 334; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 LKPSFSPNNYKALSEVOGKQMAKELARQNDLGFLLKCLAFYVNGRNIFLSPLSI 60
DB 20 LKPSFSPNNYKALSEVOGKQMAKELARQNDLGFLLKCLAFYVNGRNIFLSPLSI 79
QY 61 STAFSMLCIGADSTLDEIKQGFNRKMPKOLHGFHYIHELTKQODKLSTGNTLF 120
DB 80 STAFSMLCIGADSTLDEIKQGFNRKMPKOLHGFHYIHELTKQODKLSTGNTLF 139
QY 121 IDORLOPQRKFLBDANKFYSAETILTNFQNLMAQKQINDFISQKTHKINNLINIDPG 180
DB 140 IDORLOPQRKFLBDANKFYSAETILTNFQNLMAQKQINDFISQKTHKINNLINIDPG 199
QY 181 TWMLANTYIFFRARWKEHEDPNTVTEDEPFLEKNSSVKYPMMFRSGIYQGYDDKLSCTI 240

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DB 200 TMLLANYIFRRARKHEFPDNTKEDFPLEKNSVYKVMFRRSGIYQVYDGLKSTCTI 259
QY 241 LEIPYQKNITAIPIPLPEEGKLKHLKGLQVDTFSRKMTLLSRVVDVSVRLHMTGFDL 300
DB 260 LEIPYQKNITAIPIPLPEEGKLKHLKGLQVDTFSRKMTLLSRVVDVSVRLHMTGFDL 319
QY 301 KKTLSYIGVSKIFEEHGDLTAKIAPHRSKLVGEAV 334
DB 320 KKTLSYIGVSKIFEEHGDLTAKIAPHRSKLVGEAV 353

RESULT 9
AAU05759
AAU05759 standard; protein; 358 AA.
AAU05759;
24-OCT-2001 (first entry)
Human NOV7 polypeptide #2.
Human NOV7 polypeptide #2.
Human NOV7; A1132990 B; fertility disorder; spermatogenesis; cardiac;
cytostatic; immunomodulatory; antiproliferative; antidiabetic;
cell proliferation; cancer; diabetic retinopathy; angiogenic disorder;
pulmonary disorder; hematopoietic disorder; immunological disorder;
inflammatory disorder; tumour related disorders; emphysema; cirrhosis;
wound healing; gene therapy.
Homo sapiens.
Key Location/Qualifiers
Misc-difference 311..322
/label= OTHER
/note= "Other- Unknown"
W0200149729-A2.
12-JUL-2001.
05-JAN-2001; 2001WO-US000299.
06-JAN-2000; 2000US-0174724P.
11-JAN-2000; 2000US-0175434P.
11-JAN-2000; 2000US-0175488P.
12-JAN-2000; 2000US-0175696P.
12-JAN-2000; 2000US-0175743P.
13-JAN-2000; 2000US-0175819P.
07-AUG-2000; 2000US-0223524P.
04-JAN-2001; 2001US-0075565P.
(CURA-) CURAGEN CORP.
Prayaga SK, Majumder K, Tallon BE, Spaderna SK, Spytek KA;
Macedougall J;
WPI; 2001-418356/44.
Nucleic acids encoding polypeptides, designated NOVX polypeptides, useful
for treating a syndrome associated with a NOVX-associated disorder, e.g.
cell proliferation (e.g. cancer and diabetic retinopathy), angiogenic or
pulmonary disorder.
Disclosure; Page 33; 14pp; English.
The invention relates to nucleic acids encoding NOVX (X being an integer
from 1-8) polypeptides. The NOVX nucleic acids and polypeptides are
useful in diagnosing, treating or manufacturing a medicament for a
disease or disorder associated with NOVX e.g. cell proliferation (cancer
and diabetic retinopathy), angiogenic or pulmonary disorders, fertility
disorders (e.g. of spermatogenesis), hematopoietic, immunological,
inflammatory and tumour related disorders, emphysema, cirrhosis, wound
healing. NOVX nucleic acids are also useful in gene therapy. They are
also used for screening for a modulator of activity or of latency or

CC predisposition to a NOVX-associated disorder. They are also useful for
CC determining the presence of or predisposition to a NOVX-associated
CC disorder. The present sequence represents a version of NOV7 (A1132990 B)
CC appearing in table 25 of the specification, which has sequence homology
CC to an unidentified human secreted protein (HWHGUS54) and to alpha anti-
CC trypsin
XX
SQ Sequence 358 AA;
Query Match 78.5%; Score 310; DB 4; Length 358;
Best Local Similarity 100.0%; Pred. No. 1.4e-299;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 35 DLGFKLLKLAAPNPGRNIFLSPSTSTAPSMCLGADOSTLDEIRGFNFRMPKEDLH 94
DB 1 DLGFKLLKLAAPNPGRNIFLSPSTSTAPSMCLGADOSTLDEIRGFNFRMPKEDLH 60
QY 95 EGFHYIHLTQKTDKLSIGNTLFDLQRLQPKRFLDANKFYSAFTLTNFOULEMA 154
DB 61 EGFHYIHLTQKTDKLSIGNTLFDLQRLQPKRFLDANKFYSAFTLTNFOULEMA 120
QY 155 OKQINDPISQKTKGKTNNTLNIENIDPGTWMLANIYIFRRARKHEFPDNTKEDFPLEKN 214
DB 121 OKQINDPISQKTKGKTNNTLNIENIDPGTWMLANIYIFRRARKHEFPDNTKEDFPLEKN 180
QY 215 SSVKVPMMFRSGIYQVYDGLKSTCTLEIPIYQKNITAIPIPLPEEGKLKHLKGLQVDTFS 274
DB 181 SSVKVPMMFRSGIYQVYDGLKSTCTLEIPIYQKNITAIPIPLPEEGKLKHLKGLQVDTFS 240
QY 275 RKMTLLSRVVDVSVRLHMTGFDLAKTLLSYIGVSKIFEEHGDLTAKIAPHRSKLVGEAV 334
DB 241 RKMTLLSRVVDVSVRLHMTGFDLAKTLLSYIGVSKIFEEHGDLTAKIAPHRSKLVGEAV 300
QY 335 HKAEELMDER 344
DB 301 HKAEELMDER 310

RESULT 10
ABB11832
ID ABB11832 standard; peptide; 431 AA.
XX
AC ABB11832;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human secreted protein homologue, SEQ ID NO:2202.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; chromolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; hematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antidiabetic; antiarthritic; haemostatic; antidiabetic;
KW cytostatic; osteopathic; vasotropic; cardiac; virucide; antibacterial;
KW antifungal; vulnery; antitumor.
OS Homo sapiens.
XX
XX
PN W0200157188-A2.
XX
XX 09-AUG-2001.
XX
PD 05-FEB-2001; 2001WO-US003800.
XX
PF 03-FEB-2000; 2000US-00496914.
XX
PR 27-APR-2000; 2000US-00560875.
XX

(HYSEQ INC.
Tang YT, Liu C, Drmanac RT;
WPI, 2001-457740/49.
N-PSDB; ABA09076.
Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer.
Claim 20; Page 263; 1963jp; English.
Sequences ABA010981-ABA01330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haematopoietic regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention

Sequence 431 AA;
Query Match 43.0%; Score 170; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 4.3e-160; Indels 0; Gaps 0
Matches 170; Conservative 0; Mismatches 43; Indels 0; Gaps 0

165 KTHGKINMLIENIDGVTWLLANTYFFRRMRGHEFDPNVTKDEDFLEKNSSVKPMMPR 224
Db KTHGKINMLIENIDGVTWLLANTYFFRRMRGHEFDPNVTKDEDFLEKNSSVKPMMPR 260
201 KTHGKINMLIENIDGVTWLLANTYFFRRMRGHEFDPNVTKDEDFLEKNSSVKPMMPR 260
225 SGIYGVGYDDKLSCTILBIPYQKNITAFILPDEGKLKLEKGLQVDFSRKTTLSRRV 284
Db SGIYGVGYDDKLSCTILBIPYQKNITAFILPDEGKLKLEKGLQVDFSRKTTLSRRV 320
261 SGIYGVGYDDKLSCTILBIPYQKNITAFILPDEGKLKLEKGLQVDFSRKTTLSRRV 320
285 VDVSVPRLAMGTGTPDLKTLSTLYGYSKIPFEHGDLTAKIAPHSLKVGNAV 334
Db VDVSVPRLAMGTGTPDLKTLSTLYGYSKIPFEHGDLTAKIAPHSLKVGNAV 370

RESULT 11
AAAT79882
ID AAT79882 standard; protein; 431 AA.

XX	AAM79882;
AC	06-NOV-2001 (first entry)
DT	Human protein SEQ ID NO 3528.
XX	
DE	Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
KW	Homo sapiens.
XX	
OS	WO200157190-A2.
XX	
PD	09-AUG-2001.
XX	
PF	05-FEB-2001; 2001MO-US004098.
XX	
PR	03-FEB-2000; 2000US-00496914. 27-APR-2000; 2000US-00560875. 20-JUN-2000; 2000US-00598075. 19-JUL-2000; 2000US-00620325. 01-SEP-2000; 2000US-00654935. 15-SEP-2000; 2000US-00663561. 20-OCT-2000; 2000US-00693325. 30-NOV-2000; 2000US-00728422.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
P1	Tang YT, Liu C, Dmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Xue AJ, Yang Y, Wejhrman T, Goodrich R; WPI: 2001-476283/51. N-PDSB; AAK53015.
DR	
XX	
PT	Nucleic acids encoding polypeptides wltch cytokine-like activities, useful in diagnosis and gene therapy.
PS	Claim 20; Page 371; 6221pp; English.
CC	The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polipeptides (AAM78323-AAH80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK55581), 2111 (AAK55582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
SQ	Sequence 431 AA:
Query Match	43.0%; Score 170; DB 4; Length 431;
Best Local Similarity	100.0%; Pred. No. 4.3e-160;
Matches 170; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	165 KTHGKNNLNLEINIDGTWLLANLYFFPARMKHEPDPVTKEEDFFLEKNSSVAVPMMPF 224
Db	201 KTHGKNNLNLENIDGTWLLANLYFFPARMKHEPDPVTKEEDFFLEKNSSVAVPMMPF 260
OY	225 SGIYGVGYDDKSCSTLIEPYOKNTAIFILPDEGKLKHLEKGLOVDTFSRMKTLLSRRV 284
Db	261 SGIYGVGYDDKSCSTLIEPYOKNTAIFILPDEGKLKHLEKGLOVDTFSRMKTLLSRRV 320
OY	285 VDVSVPRLMTGTFLDKTLTSLTYIGSVKIPEEHGDLTKIAPRSIRKGEAV 334

Db 321 VDVSVPRLHMTGTEDLTKTSLYIGVSKIPEEHGDLTKIAPHRSLKVGRAV 370

RESULT 12

AAM70426
ID AAM70426 standard; protein; 140 AA.

AC AAM70426;

DT 06-NOV-2001 (first entry)

XX Human bone marrow expressed probe encoded protein SEQ ID NO: 30732.

XX Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

PN W0200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001MO-US000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLR-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human bone marrow.

XX Example 4; SEQ ID NO 30732; 658pp + Sequence listing; English.

XX The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

XX bone marrow. They can be used to measure gene expression in bone marrow

XX samples, which may enable the improved diagnosis and treatment of cancers

XX such as lymphoma, leukaemia and myeloma. The present sequence is a

XX protein encoded by one of the probes of the invention

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Sequence 140 AA;

Query Match 32.7%; Score 129; DB 4; Length 140;

Best Local Similarity 100.0%; Pred. No. 1.1e-119;

Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 FSNLCGAGDSTDEIKQGFNFRMPKDLHEGFYIHELTKOTODLKSIGNTLPIDQ 123

DB 1 FSNLCGAGDSTDEIKQGFNFRMPKDLHEGFYIHELTKOTODLKSIGNTLPIDQ 60

QY 124 RLQPORFLEDAKRFYSAEITLTNPNLENAKOINDFISQKTHGKINNIENIDPQTM 183

DB 61 RLQPORFLEDAKRFYSAEITLTNPNLENAKOINDFISQKTHGKINNIENIDPQTM 120

QY 184 LLANYTFPR 192

DB 121 LLANYTFPR 129

Search completed: March 31, 2006, 10:02:30
Job time : 212.427 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2006, 10:02:58 ; Search time 24.9011 Seconds
(without alignments)
1526.262 Million cell updates/sec

Title: US-10-664-356-1562_COPY_20_414
Perfect score: 395
Sequence: 1 ILKPSFSPRYKALSRVQGW.....YSEKIPSVLFGKIVNPYIGK 395

Scoring table: ORIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 15

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : PIR_80: +
1: p1r1: +
2: p1r2: +
3: p1r3: +
4: p1r4: +

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	ID	Description
------------	-------------	----	-------------

No matches found

Search completed: March 31, 2006, 10:08:39
Job time : 24.9011 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using SW model

Run on: March 31, 2006, 09:55:21 ; Search time 149.895 Seconds
(without alignments)
1859.193 Million cell updates/sec

Title: US-10-664-356-1562_COPY_20_414
Perfect score: 395
Sequence: 1 LKPSFSPRYKALSEVQW.....YSEKIPSVLFGKIYVPIGK 395

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size: 15

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 500 summaries

Database : UniProt_05.80:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	395	100.0	414	Q81W75_HUMAN	Q81W75 homo sapien
2	19	4.8	413	Q7TWF5_MOUSE	Q7TWF5 mus musculu
3	19	4.8	413	Q9CGJ2_MOUSE	Q9CGJ2 m mus muscu
4	19	4.8	413	Q6P6M3_MOUSE	Q6P6M3 mus musculu
5	16	4.1	411	Q8R4Z1_RAT	Q8R4Z1 rattus norv

ALIGNMENTS

RESULT 1
Q81W75_HUMAN
ID Q81W75_HUMAN PRELIMINARY; PRT; 414 AA.
AC Q81W75;
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Serine (Or cysteine) proteinase inhibitor, clade A (Alpha-1
DE antiproteinase, antitrypsin), member 12 (Ol-64) (Visceral adipose-
DE specific SERPIN)
GN Name=SERPIN12;
OS Homo sapiens (human).
OC Bkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
OC Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Foley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.B., Jones S.U.M., Maira M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Skin;
RG NIH WGC Project;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RN NUCLEOTIDE SEQUENCE.
RA Hida K., Wada J., Zhang H.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1. SIMILARITY: Belongs to the serpin family.
DR EMBL; BC040857; AA040857.1; -; mRNA.
DR EMBL; AY177692; AA018649.1; -; mRNA.
DR EMBL; AY326420; AAP8384.1; -; mRNA.
DR HSSP; P01009; IOMB.
DR Ensembl; ENSG00000165953; Homo sapiens.
DR HGNC; HGNC:18359; SERPIN12.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
KW Serpin.
SQ SEQUENCE 414 AA; 47175 MW; 5C70F1AB5935661C CRC64;
Query Match 100.0%; Score 395; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LKPSFSPRYKALSEVQWKMMAKELARQNMIDGFKLLKKLAFFNPGNIFLSPLSI 60
DB 20 LKPSFSPRYKALSEVQWKMMAKELARQNMIDGFKLLKKLAFFNPGNIFLSPLSI 79
QY 61 STAFSMCLGAOSTLDEIKQGFNFRMPKDIABGHYIHLTQTOOLKISGNTLF 120
DB 80 STAFSMCLGAOSTLDEIKQGFNFRMPKDIABGHYIHLTQTOOLKISGNTLF 139
QY 121 IDPRLPQRFLEADAKNFYSATLITNFQNLMAQKQINDFISQTHGKINNLIENIDPG 180
DB 140 IDPRLPQRFLEADAKNFYSATLITNFQNLMAQKQINDFISQTHGKINNLIENIDPG 199
QY 181 TWMLLANYFFRRARWTHGEPDNTYKEEDFLEKSSVVKPMFRSGIYGVYDLSCTI 240
DB 200 TWMLLANYFFRRARWTHGEPDNTYKEEDFLEKSSVVKPMFRSGIYGVYDLSCTI 259
QY 241 LRIPIYQKNTAIFILDEGLKLEKGLQVDTSSRKITLSRVNDVSVRLMTGFDL 300
DB 260 LRIPIYQKNTAIFILDEGLKLEKGLQVDTSSRKITLSRVNDVSVRLMTGFDL 319
QY 301 KKTLSYIGVSKLFEHGDTLTKLAPHRSLKVGAVHKAELKMDRGTEGAAGTQTLPM 360

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Db      320 KKTLSYIGVSKIFEBHGDLTAKIAPHRSKVGAEVHKAELKMDERGTGGAAGTAPME 379
Qy      361 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 395
Db      380 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414

RESULT 2
Q7TMFS MOUSE PRELIMINARY; PRT; 413 AA.
AC      07TMFS_
DT      01-OCT-2003 (TEMBLrel. 25, Created)
DT      01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DE      01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE      Visceral adipose-specific SERPIN.
GN      Name=Serpin12;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=Swiss Webster;
RA      Hida K., Wada J., Zhang H.;
RL      Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: Belongs to the serpin family.
DR      EMBL; AY326419; AAP88383.1; -; mRNA.
DR      HSSP; P01008; 1ATH.
DR      MGI; MGI:1915304; Serpin12.
DR      GO; GO:0005615; Extracellular space; TAS.
DR      InterPro; IPR000295; Proc_inh_Leerp2.
DR      InterPro; IPR000215; Proc_inh_serpin.
DR      Pfam; PF00079; Serpin; 1.
DR      PRINTS; PR00780; LEUSERPINII.
DR      SMART; SM00093; SERPIN; 1.
DR      PROSITE; PS00284; SERPIN; 1.
SQ      SEQUENCE 413 AA; 47674 MW; EE2B3B08C2DD418F CRC64;

Query Match 4.8%; Score 19; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      325 HRSKVGAEVHKAELKMD 343
Db      344 HRSKVGAEVHKAELKMD 362

RESULT 3
Q9CQ32 MOUSE PRELIMINARY; PRT; 413 AA.
AC      Q9CQ32;
DT      01-JUN-2001 (TEMBLrel. 17, Created)
DT      01-JUN-2001 (TEMBLrel. 17, Last sequence update)
DT      01-FEB-2005 (TEMBLrel. 29, Last annotation update)
DE      Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched
DE      library, clone:4632419J12 product:hypothetical Serpins containing
DE      protein, full insert sequence (Mus musculus 17 days embryo head cDNA,
DE      RIKEN full-length enriched library, clone:3300001F13
DE      product:hypothetical Serpins containing protein, full insert
DE      sequence).
GN      Name=Serpin12;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX      MEDLINE=57979253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RX      Carninci P., Hayashizaki Y.;

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RT      "High-efficiency full-length cDNA cloning.";
RL      Mech. Enzymol. 303:19-44(1999).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX      MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA      Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA      Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA      Saito T., Okazaki Y., Gojobori T., Bono H., Kanakawa T., Saito R.,
RA      Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Glast C., King B., Kochiwa H.,
RA      Kuehl P., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J.,
RA      Schriml L.M., Stambli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Bash G.,
RA      Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA      Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA      Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohseki S.,
RA      Hayashizaki Y.;
RT      "Functional annotation of a full-length mouse cDNA collection.";
RL      Nature 409:685-690(2001).
RN      [3]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX      MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA      Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA      Nagai K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA      Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA      Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA      Blake J.A., Brad D., Brusic V., Chotila C., Corbani L.B., Cousins S.,
RA      Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA      Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA      Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA      Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA      Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA      Maglott D.R., Maltale L., Marchionni L., McKenzie L., Miki H.,
RA      Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
RA      Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA      Ravaei T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA      Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA      Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA      Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA      Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,
RA      Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA      Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA      Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA      Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA      Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA      Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA      Birney E., Hayashizaki Y.;
RT      "Analyses of the mouse transcriptome based on functional annotation of
RT      60,770 full-length cDNAs.";
RL      Nature 420:563-573(2002).
RN      [4]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX      MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA      Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA      Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT      "Normalization and subtraction of cap-trapper-selected cDNAs to
RT      prepare full-length cDNA libraries for rapid discovery of new genes.";
RL      Genome Res. 10:1617-1630(2000).
RN      [5]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RX      MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA      Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

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RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6].
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head, and Skin;
RA Adachi J., Mizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Hanakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hasegaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Horii F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tojima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL: AK014589; BAB29447.1; -; mRNA.
DR EMBL: AK014346; BAB29287.1; -; mRNA.
DR HSSP: P01008; IATH.
DR Ensemble: ENSMUSG0000041567; Mus musculus.
DR MGI: MGI:1915304; Serpin12.
DR GO: GO:0005615; C:extracellular space; TAS.
DR InterPro: IPR000295; Prot_inh_lsepr2.
DR InterPro: IPR000215; Prot_inh_serpin.
DR Pfam: PF00079; Serpin_1.
DR PRINTS: PR00780; LEUSERPIN1.
DR SMART: SM00093; SERPIN; 1.
DR PROSITE: PS00284; SERPIN; 1.
DR Hypothetical protein.
DR KW SEQUENCE 413 AA; 47634 MW; DOA8B1BE24FD60A CRC64;
SO
Query Match 4.8%; Score 19; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 325 HRSLLKGEAVHAKELKMD 343
DB 344 HRSLLKGEAVHAKELKMD 362

RESULT 4
06P6M3_MOUSE PRELIMINARY; PRT; 413 AA.
AC 06P6M3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Visceral adipose-specific SERPIN.
GN Name=Serpin12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1].
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Jaw and Limb;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hightower R.F., Jordan H., Moore T., Max S.I., Wang J.F.,
RA Diatchenko L., Marisla K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguanello N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McBurn P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.B., Jones S.J.M., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2].
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Jaw and Limb;
RG NIH MGC Project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL: BC062143; AA62143.1; -; mRNA.
DR HSSP: P01008; IATH.
DR Ensemble: ENSMUSG0000041567; Mus musculus.
DR MGI: MGI:1915304; Serpin12.
DR GO: GO:0005615; C:extracellular space; TAS.
DR InterPro: IPR000295; Prot_inh_lsepr2.
DR InterPro: IPR000215; Prot_inh_serpin.
DR Pfam: PF00079; Serpin_1.
DR PRINTS: PR00780; LEUSERPIN1.
DR SMART: SM00093; SERPIN; 1.
DR PROSITE: PS00284; SERPIN; UNKNOWN_1.
DR KW SEQUENCE 413 AA; 47630 MW; CE1940BA2EB35811 CRC64;
SO
Query Match 4.8%; Score 19; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 325 HRSLLKGEAVHAKELKMD 343
DB 344 HRSLLKGEAVHAKELKMD 362

RESULT 5
08R4Z1_RAT PRELIMINARY; PRT; 411 AA.
AC 08R4Z1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Visceral adipose tissue specific SERPIN.
GN Name=Serpin12; Synonyms=Vaspin;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1].
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OLETF; TISSUE=Visceral adipose;
RA Hida K., Wada J., Zhang H., Shikata K., Makino H.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the serpin family.
DR EMBL: AF245398; AAU9574.1; -; mRNA.
DR HSSP: P01008; IATH.
DR Ensemble: ENSRNOG00000009710; Rattus norvegicus.
DR RGD: 708485; Serpin12.
DR GO: GO:0004677; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro: IPR000295; Prot_inh_lsepr2.
DR InterPro: IPR000215; Prot_inh_serpin.
DR Pfam: PF00079; Serpin_1.
DR PRINTS: PR00780; LEUSERPIN1.
DR SMART: SM00093; SERPIN; 1.

KW Serpin. 411 AA; 47527 MW; 29FA271FF8CC8A2D CRC64;
SQ SEQUENCE

Query Match 4.1%; Score 16; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 NIFLSPPLSISTAFSML 67

DB 71 NIFLSPPLSISTAFSML 86

Search completed: March 31, 2006, 10:07:43
Job time : 149.895 secs

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 31, 2006, 10:08:07 ; Search time 32.225 seconds
(without alignments)
1013.403 Million cell updates/sec

Title: US-10-664-356-1562_COPY_20_414

Perfect score: 395

Sequence: 1 LKPSFSPRYKALSEVQGM.....YSEKIPSVLFLGKIYNPICK 395

Scoring table: OLIGO

Gapop 60.0, Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 7

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 500 summaries

Database : Issued Patents AA:

1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCJUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	395	100.0	414	2	US-09-755-665-14
2	395	100.0	414	2	US-09-755-665-55
3	395	100.0	414	2	US-09-755-665-56
4	395	100.0	415	2	US-09-461-325-134
5	395	100.0	415	2	US-10-012-542-134
6	395	100.0	415	2	US-10-115-123-134
7	310	78.5	361	2	US-09-755-665-57

ALIGNMENTS

RESULT 1
US-09-755-665-14
Sequence 14, Application US/09755665
Patent No. 6600019
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhiradas K.
APPLICANT: Majumder, Kunud
APPLICANT: Tallon, Bruce B.
APPLICANT: Spaderma, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14

PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-09-755-665-14

Query Match 100.0%; Score 395; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LLKPSFSPRYKALSEVQGMQRMAAKELARQNDLGFKLKLAFLNPRGRIFLSPISI	60
DB	20	LLKPSFSPRYKALSEVQGMQRMAAKELARQNDLGFKLKLAFLNPRGRIFLSPISI	79
QY	61	STAFSMLCLGADSTLDEIKGFNFRKPEKDLHGFYIITHELTQTKDGLSTGNTLF	120
DB	80	STAFSMLCLGADSTLDEIKGFNFRKPEKDLHGFYIITHELTQTKDGLSTGNTLF	139
QY	121	IDRLQPKRKLADAKNFSAETLLTNFQNLMAQKQINDPISQKTHKINNLENDPG	180
DB	140	IDRLQPKRKLADAKNFSAETLLTNFQNLMAQKQINDPISQKTHKINNLENDPG	199
QY	181	TVMLLANYIFFRAMKHEFDNVTKEEDPFLEKNSYKVPMMFRSGIYQVGYDGLSCTI	240
DB	200	TVMLLANYIFFRAMKHEFDNVTKEEDPFLEKNSYKVPMMFRSGIYQVGYDGLSCTI	259
QY	241	LEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWMTLSRRVVDVSPRLHMTGTEDL	300
DB	260	LEIPYQKNITAFILPDEGKLKLEKGLQVDTFSRWMTLSRRVVDVSPRLHMTGTEDL	319
QY	301	KKTLSTYIGVSKIFREHGLTKIAPHSILKVEAVHAKELKXDERGTGAGTGAQTLPME	360
DB	320	KKTLSTYIGVSKIFREHGLTKIAPHSILKVEAVHAKELKXDERGTGAGTGAQTLPME	379
QY	361	TPLVVXKIDKPYLLIYSEKIPSVLFLGKIYNPICK	395
DB	380	TPLVVXKIDKPYLLIYSEKIPSVLFLGKIYNPICK	414

RESULT 2
US-09-755-665-55
Sequence 55, Application US/09755665
Patent No. 6600019
GENERAL INFORMATION:
APPLICANT: Prayaga, Sudhiradas K.
APPLICANT: Majumder, Kunud
APPLICANT: Tallon, Bruce B.
APPLICANT: Spaderma, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: MacDougall, John
TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-631
CURRENT APPLICATION NUMBER: US/09/755,665
CURRENT FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 55
LENGTH: 414
TYPE: PRT
ORGANISM: Homo sapiens
US-09-755-665-55

Query Match 100.0%; Score 395; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LKPSFSPRYKALSEVQGMQRMAAKELARQNDLGFKLKLAFLNPRGRIFLSPISI 60

Db 20 LKPSFSPRYKALSEVQGWKQMAKELARQNMNDLGFLLKCLAFYNGRNIFLSPLSI 79
Qy 61 STAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHEGFHYIHELTOXTODLKLISGNTLF 120
Db 80 STAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHEGFHYIHELTOXTODLKLISGNTLF 139
Qy 121 IDORLOPQKFLLEDANKFYSAETITLTFNFOLEMAQKQINDFISQKTHGKINNLLENIDPG 180
Db 140 IDORLOPQKFLLEDANKFYSAETITLTFNFOLEMAQKQINDFISQKTHGKINNLLENIDPG 199
Qy 181 TWMLLANYIFFRARMKHEPDVNTKEEDFLEKSSVVKVPMFRSGIYGVYDDKLSCTI 240
Db 200 TWMLLANYIFFRARMKHEPDVNTKEEDFLEKSSVVKVPMFRSGIYGVYDDKLSCTI 259
Qy 241 LEIPYQKNITAFILPDEBGLKHLKGLQVDTFSRWKTLSSRRVVDVSVRLHMTGTFDL 300
Db 260 LEIPYQKNITAFILPDEBGLKHLKGLQVDTFSRWKTLSSRRVVDVSVRLHMTGTFDL 319
Qy 301 KKTLSYIGVSKIFEEHGDLTFLAPHRSLKVGAVHKAELKMDERGTEGAAGTGAQTLPM 360
Db 320 KKTLSYIGVSKIFEEHGDLTFLAPHRSLKVGAVHKAELKMDERGTEGAAGTGAQTLPM 379
Qy 361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIYVPIGK 395
Db 380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIYVPIGK 414

RESULT 3

US-09-755-665-56
; Sequence 56, Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce B.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-755-665-56

Query Match 100.0%; Score 395; DB 2; Length 414;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPSFSPRYKALSEVQGWKQMAKELARQNMNDLGFLLKCLAFYNGRNIFLSPLSI 60
Db 20 LKPSFSPRYKALSEVQGWKQMAKELARQNMNDLGFLLKCLAFYNGRNIFLSPLSI 79
Qy 61 STAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHEGFHYIHELTOXTODLKLISGNTLF 120
Db 80 STAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHEGFHYIHELTOXTODLKLISGNTLF 139
Qy 121 IDORLOPQKFLLEDANKFYSAETITLTFNFOLEMAQKQINDFISQKTHGKINNLLENIDPG 180
Db 140 IDORLOPQKFLLEDANKFYSAETITLTFNFOLEMAQKQINDFISQKTHGKINNLLENIDPG 199
Qy 181 TWMLLANYIFFRARMKHEPDVNTKEEDFLEKSSVVKVPMFRSGIYGVYDDKLSCTI 240
Db 200 TWMLLANYIFFRARMKHEPDVNTKEEDFLEKSSVVKVPMFRSGIYGVYDDKLSCTI 259

Qy 241 LEIPYQKNITAFILPDEBGLKHLKGLQVDTFSRWKTLSSRRVVDVSVRLHMTGTFDL 300
Db 260 LEIPYQKNITAFILPDEBGLKHLKGLQVDTFSRWKTLSSRRVVDVSVRLHMTGTFDL 319
Qy 301 KKTLSYIGVSKIFEEHGDLTFLAPHRSLKVGAVHKAELKMDERGTEGAAGTGAQTLPM 360
Db 320 KKTLSYIGVSKIFEEHGDLTFLAPHRSLKVGAVHKAELKMDERGTEGAAGTGAQTLPM 379
Qy 361 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIYVPIGK 395
Db 380 TPLVVKIDKPYLLLIYSEKIPSVLFLGKIYVPIGK 414

RESULT 4

US-09-461-325-134
; Sequence 134, Application US/09461325A
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-09-461-325-134

Query Match 100.0%; Score 395; DB 2; Length 415;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKPSFSPRYKALSEVQGWKQMAKELARQNMNDLGFLLKCLAFYNGRNIFLSPLSI 60
Db 20 LKPSFSPRYKALSEVQGWKQMAKELARQNMNDLGFLLKCLAFYNGRNIFLSPLSI 79
Qy 61 STAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHEGFHYIHELTOXTODLKLISGNTLF 120
Db 80 STAFSMLCLGAODSTLDEIKQGFNFRKMPKEDLHEGFHYIHELTOXTODLKLISGNTLF 139
Qy 121 IDORLOPQKFLLEDANKFYSAETITLTFNFOLEMAQKQINDFISQKTHGKINNLLENIDPG 180
Db 140 IDORLOPQKFLLEDANKFYSAETITLTFNFOLEMAQKQINDFISQKTHGKINNLLENIDPG 199
Qy 181 TWMLLANYIFFRARMKHEPDVNTKEEDFLEKSSVVKVPMFRSGIYGVYDDKLSCTI 240
Db 200 TWMLLANYIFFRARMKHEPDVNTKEEDFLEKSSVVKVPMFRSGIYGVYDDKLSCTI 259
Qy 241 LEIPYQKNITAFILPDEBGLKHLKGLQVDTFSRWKTLSSRRVVDVSVRLHMTGTFDL 300
Db 260 LEIPYQKNITAFILPDEBGLKHLKGLQVDTFSRWKTLSSRRVVDVSVRLHMTGTFDL 319

QY 301 KKTLSYIGVSKIPFEEHGDLTAKAPHRSLKVGAVHKAELKMDERGTGGAAGTGLPME 360
DB 320 KKTLSYIGVSKIPFEEHGDLTAKAPHRSLKVGAVHKAELKMDERGTGGAAGTGLPME 379
QY 361 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 395
DB 380 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414

RESULT 5

US-10-012-542-134
; Sequence 134, Application US/10012542
; Patent No. 6627741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-012-542-134

Query Match 100.0%; Score 395; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPSFSPRYKALSEVQGWKQMAAKELARQNDLGFKLLKGLAFYNGRNTFLSPLSI 60
DB 20 LKPSFSPRYKALSEVQGWKQMAAKELARQNDLGFKLLKGLAFYNGRNTFLSPLSI 79
QY 61 STAFSMLCLGAOSTLDEIKQGFNFRKMPKDLHEGFHYIIHBLTQKTODLKISGNTLF 120
DB 80 STAFSMLCLGAOSTLDEIKQGFNFRKMPKDLHEGFHYIIHBLTQKTODLKISGNTLF 139
QY 121 IDRLPQRFKFLBDANKFYSAETILTNFQULEMAQKQINDFISQTHGKINNLIENIDPG 180
DB 140 IDRLPQRFKFLBDANKFYSAETILTNFQULEMAQKQINDFISQTHGKINNLIENIDPG 199
QY 181 TWVLLANYIFFRARWKGHEFDPNVTKEEDFLEKNSSVKVPMMFRSGIYQGYDDKLSCTI 240
DB 200 TWVLLANYIFFRARWKGHEFDPNVTKEEDFLEKNSSVKVPMMFRSGIYQGYDDKLSCTI 259
QY 241 LEIPYQKNITAIIFILPDEGDKLKEKGLQVDTFSRWKTLISRVDVSVRLHMTGTFDL 300
DB 260 LEIPYQKNITAIIFILPDEGDKLKEKGLQVDTFSRWKTLISRVDVSVRLHMTGTFDL 319
QY 301 KKTLSYIGVSKIPFEEHGDLTAKAPHRSLKVGAVHKAELKMDERGTGGAAGTGLPME 360
DB 320 KKTLSYIGVSKIPFEEHGDLTAKAPHRSLKVGAVHKAELKMDERGTGGAAGTGLPME 379

QY 361 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 395
DB 380 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414

RESULT 6

US-10-115-123-134
; Sequence 134, Application US/10115123
; Patent No. 674216
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029G30APID2
; CURRENT APPLICATION NUMBER: US/10/115,123
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 134
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (415)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-115-123-134

Query Match 100.0%; Score 395; DB 2; Length 415;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LKPSFSPRYKALSEVQGWKQMAAKELARQNDLGFKLLKGLAFYNGRNTFLSPLSI 60
DB 20 LKPSFSPRYKALSEVQGWKQMAAKELARQNDLGFKLLKGLAFYNGRNTFLSPLSI 79
QY 61 STAFSMLCLGAOSTLDEIKQGFNFRKMPKDLHEGFHYIIHBLTQKTODLKISGNTLF 120
DB 80 STAFSMLCLGAOSTLDEIKQGFNFRKMPKDLHEGFHYIIHBLTQKTODLKISGNTLF 139
QY 121 IDRLPQRFKFLBDANKFYSAETILTNFQULEMAQKQINDFISQTHGKINNLIENIDPG 180
DB 140 IDRLPQRFKFLBDANKFYSAETILTNFQULEMAQKQINDFISQTHGKINNLIENIDPG 199
QY 181 TWVLLANYIFFRARWKGHEFDPNVTKEEDFLEKNSSVKVPMMFRSGIYQGYDDKLSCTI 240
DB 200 TWVLLANYIFFRARWKGHEFDPNVTKEEDFLEKNSSVKVPMMFRSGIYQGYDDKLSCTI 259
QY 241 LEIPYQKNITAIIFILPDEGDKLKEKGLQVDTFSRWKTLISRVDVSVRLHMTGTFDL 300
DB 260 LEIPYQKNITAIIFILPDEGDKLKEKGLQVDTFSRWKTLISRVDVSVRLHMTGTFDL 319
QY 301 KKTLSYIGVSKIPFEEHGDLTAKAPHRSLKVGAVHKAELKMDERGTGGAAGTGLPME 360
DB 320 KKTLSYIGVSKIPFEEHGDLTAKAPHRSLKVGAVHKAELKMDERGTGGAAGTGLPME 379
QY 361 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 395
DB 380 TPLVVKIDKPYLLIYSEKIPSVLFLGKIYVPIGK 414

RESULT 7

```
US-09-755-665-57
; Sequence 57: Application US/09755665
; Patent No. 6600019
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas K.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tailon, Bruce E.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-631
; CURRENT APPLICATION NUMBER: US/09/755,665
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/174,724
; PRIOR FILING DATE: 2000-01-06
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 361
; TYPE: PRP
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)..(361)
; OTHER INFORMATION: wherein Xaa is any amino acid as defined in the
; OTHER INFORMATION: specification
US-09-755-665-57
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Query Match 78.5%; Score 310; DB 2; Length 361;

Best Local Similarity 100.0%; Pred. No. 8.1e-294;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 35 DLGFKLLKLAFLYPPGNITLSPISISTAFSMLCLGAQDSTLDEIKGFNFRKMPKDLH 94
DB 1 DLGFKLLKLAFLYPPGNITLSPISISTAFSMLCLGAQDSTLDEIKGFNFRKMPKDLH 60
QY 95 EGFHYIHELTKTODLKLSIGNTLFDORLOPORKFLEDAKNFYSSETILTNPONLEMA 154
DB 61 EGFHYIHELTKTODLKLSIGNTLFDORLOPORKFLEDAKNFYSSETILTNPONLEMA 120
QY 155 OKQINDFISQKTGKINNLIENIDPGTVMILANYIFPRAMKHEFDPNVTKEEDFFLEKN 214
DB 121 OKQINDFISQKTGKINNLIENIDPGTVMILANYIFPRAMKHEFDPNVTKEEDFFLEKN 180
QY 215 SSVKVPMMPFRSGIYQVGYDDKLSCTILIEIPYQKNITAIPTLPDEGKLKHEKGLQVDTFS 274
DB 181 SSVKVPMMPFRSGIYQVGYDDKLSCTILIEIPYQKNITAIPTLPDEGKLKHEKGLQVDTFS 240
QY 275 RKMTLSRRVVDVSVPLHMTGTFDLKKTLSYIGVSKIPFEHGDLTAKIAPHRSLKVGAV 334
DB 241 RKMTLSRRVVDVSVPLHMTGTFDLKKTLSYIGVSKIPFEHGDLTAKIAPHRSLKVGAV 300
QY 335 HKAEILMDER 344
DB 301 HKAEILMDER 310
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